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L1             1 S ETHANOL/CN
L2             2 S XYLOSE/CN
L3             1 S L-XYLOSE/CN
L4             2 S GLUCOSE/CN
L5             1 S L-GLUCOSE/CN
               E XYLOSE REDUCTASE/CN
L6             4 S E3
L7            23 S XYLOSE REDUCTASE
L8            19 S L7 NOT L6
L9             4 S L6-L8 AND (SACCHAROMYCES OR CEREVISIAE)
L10           19 S L6-L8 NOT L9
               E XYLITOL DEHYDROGENASE/CN
L11            2 S E3
               E XYLITOL DEHYDROGENASE
L12            4 S XYLITOL DEHYDROGENASE
L13            2 S L12 NOT L11
               E XYLULOKINASE/CN
L14            1 S E3
               E XYLULOKINASE
L15           22 S XYLULOKINASE
L16           21 S L15 NOT L14
L17            2 S L16 AND (SACCHAROMYCES OR CEREVISIAE)
L18           20 S L14-L16 NOT L17

     FILE 'HCAPLUS' ENTERED AT 06:51:54 ON 18 MAR 2003
L19       144999 S L1
L20       497460 S ETOH OR ETHANOL OR ETHYLALCOHOL OR ETHYL ALCOHOL
L21        11773 S L2,L3
L22        23109 S XYLOSE
L23       141947 S L4 OR L5
L24       347783 S GLUCOSE
L25            7 S L9
L26         2495 S L10
L27          219 S L11 OR L12
L28            1 S L17
L29          151 S L18
L30         2747 S L25-L29
L31          427 S XYLOSE REDUCTASE OR XYLITOL DEHYDROGENASE OR XYLULOKINASE
L32         3209 S L19,L20 AND L21,L22
L33        19975 S L19,L20 AND L23,L24
L34          140 S L32,L33 AND L30,L31
L35           57 S L34 AND (SACCHAROMYCES OR S)()CEREVIS?
               E HO N/AU
L36           53 S E3,E11,E27,E30,E31
               E CHEN Z/AU
L37          669 S E3,E7
               E CHEN ZHENG/AU
L38          240 S E3,E4
L39            8 S E48
L40            3 S L35 AND L36-L39
               E GENETIC ENGINEERING/CT
               E E3+ALL
L41        79737 S E2+NT
L42       235194 S E1+NT
L43       105263 S E8+NT OR E10+NT OR E11+NT OR E16+NT OR E18+NT OR E19+NT
               E MOLECULAR CLONING/CT
               E E3+ALL
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                 E E9+ALL
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L46       581609 S GENET?/SC,SX
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                 E GENE/CT
L48       402103 S E3
                 E E55+ALL
L49       551720 S E1 OR E2 OR E3+NT
L50           29 S L35 AND L48,L49
                 E NUCLEIC ACIDS/CT
                 E E3+ALL
L51            2 S L35 AND E3+NT
L52            8 S L35 AND (E381+NT OR E382+NT OR E383+NT OR E384+NT OR E385+NT
                 E NUCLEIC ACID SEQUENCES/CT
                 E E4+ALL
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L55           29 S L35 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
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                 E E10+ALL
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                 E E11+ALL
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L61            4 S L55 AND L60
L62           14 S L40,L56,L61
L63           43 S L35,L54-L56,L60-L61 NOT L62
L64           15 S L63 AND L55
L65           13 S L64 AND FERMENT?/SC,SX,CW,BI
L66           27 S L62,L65
L67           30 S L63 NOT L66
L68            2 S L67 AND L55
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L70           28 S L66,L69
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L72            0 S L35 AND RIBOSOM?
L73            0 S L34 AND RIBOSOM?
L74        64238 S (S OR SACCHAROMYC?)()CEREVIS?
L75         2682 S L74 AND RIBOSOM?
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                 E RIBOSOM/CT
                 E E5+ALL
L76         2638 S E2
L77          124 S L76 AND L74
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L80           24 S L79 AND L19,L20
L81          446 S L74 AND RDNA
L82          231 S L81 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
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L84            0 S L79,L82 AND L30,L31

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FILE COVERS 1907 - 18 Mar 2003 VOL 138 ISS 12
FILE LAST UPDATED: 17 Mar 2003 (20030317/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L70 ANSWER 1 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:20039 HCAPLUS
DN 130:195810
TI Genetic improvement of yeasts for **ethanol** production from **xylose**
AU Limtong, S.; Tantirungkij, M.; Pirapatrungsuriya, K.; Chomthong, S.; Kitpreechavanich, V.; Santisopasri, W.; Nakashima, N.; Seki, T.; Yoshida, T.
CS Department of Microbiology, Faculty of Science, Kasetsart University, Bangkok, Thailand
SO Biotechnology for Sustainable Utilization of Biological Resources in the Tropics (**1997**), 11, 80-86
CODEN: BSUTFT
PB Osaka University, International Center for Biotechnology
DT Journal
LA English
CC 16-5 (**Fermentation** and Bioindustrial Chemistry)
AB Genetics of P. stipitis CBS5773 was manipulated by mutation. The selected mutant, S-L-100, showed increasing in **ethanol** prodn. from **xylose** both **ethanol** concn. and yield. The construction of fusants possessed high ability of **ethanol** prodn. from **xylose** by intraspecific protoplast fusion of P. stipitis CBS5773 and intergeneric protoplast fusion of Pichia stipitis CBS5773 and **Saccharomyces cerevisiae** AM12 was carried out. The fusant, FS198, derived from intraspecific hybridization showed highest **ethanol** prodn. from **xylose**. FG101 was the best fusant from intergeneric cross. Both fusants produced **ethanol** from **xylose** with higher concn. and yield and demonstrated higher **xylose reductase** and **xylitol dehydrogenase** activities than P. stipitis CBS5773. The intraspecific fusant revealed very high stability when compared with the intergeneric fusant. Also we reported the construction of **xylose** assimilating recombinant **S. cerevisiae** that could produce **ethanol** from both **xylose** and **glucose** by introduction of the genes encoding **xylose reductase** and **xylitol dehydrogenase** from P. stipitis CBS5773.
ST **ethanol fermn** Pichia Saccharomyces protoplast fusion
IT **Saccharomyces cerevisiae**
Yamadazyma stipitis
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)

IT Cell fusion
(protoplast; genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(**fermentation**; genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
IT **9028-16-4**, NAD-dependent **xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Barnett, J; Adv Carbohydr Chem Biochem 1976, V32, P126
(2) Bruinenberg, P; Appl Microbiol Biotechnol 1984, V19, P256 HCAPLUS
(3) Dellweg, H; Biotechnol Lett 1984, V6, P395 HCAPLUS
(4) Du Preez, J; Biotechnol Lett 1983, V5, P357 HCAPLUS
(5) Gong, C; Biotechnol Bioeng 1983, V25, P85 HCAPLUS
(6) Jeffries, T; Trends Biotechnol 1985, V3, P208 HCAPLUS
(7) Laplace, J; Biotechnol Lett 1991, V13, P445 HCAPLUS
(8) Maleszka, R; Appl Environ Microbiol 1982, V44(4), P909 HCAPLUS
(9) Oshima, T; Genetic 1980, V94, P841
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(11) Schneider, H; Biotechnol Lett 1981, V3, P89 HCAPLUS
(12) Schneider, H; CRC Crit Rev Biochem Mol Biol 1989, V9, P1 HCAPLUS
(13) Seki, T; Biotechnol Lett 1983, V5, P351 HCAPLUS
(14) Slininger, P; Biotechnol and Bioeng 1982, V14, P371
(15) Slininger, P; Enzyme Microb Technol 1987, P5 HCAPLUS
(16) Tantirungkij, M; J Ferment Bioeng 1993, V75, P83 HCAPLUS
(17) Wong, K; Microbiol Rev 1988, V52, P305 HCAPLUS
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(**fermentation**; genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **9028-16-4**, NAD-dependent **xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

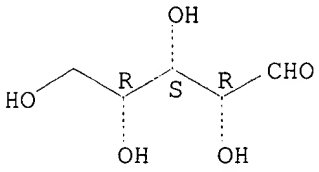
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(genetic improvement of yeasts for **ethanol** prodn. from **xylose**)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 2 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1998:415433 HCAPLUS
DN 129:226583
TI Effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes
AU Bao, Xiaoming; Gao, Dong; Qu, Yinbo; Wang, Zunong
CS Department of Microbiology, State Key Lab of Microbial Technology, Shandong University, Jinan, 250100, Peop. Rep. China
SO Shengwu Gongcheng Xuebao (**1997**), 13(4), 355-361
CODEN: SGXUED; ISSN: 1000-3061
PB Kexue Chubanshe
DT Journal
LA Chinese
CC 3-6 (Biochemical **Genetics**)
Section cross-reference(s): 10
AB **Saccharomyces cerevisiae** was transformed with the Pichia stipitis CBS6054 XYL1 and XYL2 genes encoding **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH), resp. The XYL1 and XYL2 genes were placed under the control of the alc. dehydrogenase 1 (ADH1) and phosphoglycerate kinase (PGK) promoter and inserted into the yeast plasmid YEp24. Different recombinant **S. cerevisiae** were constructed resulting in different specific activities of XR and XDH. The highest XR or XDH activities were obtained when the expressed gene was controlled by the PGK promoter and located

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downstream of ADH1 promoter-gene-terminator sequence. The XR/XDH ratio(ratio of specific enzyme activities of XR and XDH) in those recombinant **S.cerevisiae** strains varied from 17.5 to 0.06. To enhance **xylose** utilization in the XYL1, XYL2 contg. **S. cerevisiaes** strains, the native TKL1 gene encoding transketolase and TAL1 gene encoding transaldolase were also over-expressed, which showed considerably good growth on **xylose** plate. Fermn. of the recombinant **S. cerevisiae** strains contg. XYL1, XYL2, TKL1 and TAL1 were studied in mixts. of **glucose** and **xylose**. The strain with an XR/XDH ratio of 0.06 consumed 3.25 g/L **xylose** and formed no xylitol and less glycerol and acetic acid, but produced more **ethanol** compared with the higher XR/XDH ratio strain.

ST Saccharomyces **xylose** metab gene **ethanol** formation

IT **Gene, microbial**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(TAL1; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **Gene, microbial**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(TKL1; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **Gene, microbial**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(XYL1; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **Gene, microbial**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(XYL2; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **Saccharomyces cerevisiae**
(effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **9028-16-4, Xylitol dehydrogenase**
9028-31-3, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **58-86-6, Xylose**, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT 9014-46-4, Transaldolase 9014-48-6, Transketolase
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(expression of; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **64-17-5P, Ethanol**, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)

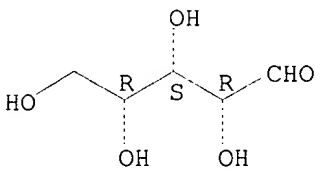
(formation of; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)

IT **9028-16-4, Xylitol dehydrogenase**
9028-31-3, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 9028-31-3 HCAPLUS
CN Reductase, aldose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6, Xylose**, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **64-17-5P, Ethanol**, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(formation of; effect on product formation in recombinant **Saccharomyces cerevisiae** expressing different level of **xylose** metabolic genes)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

L70 ANSWER 3 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:746143 HCAPLUS
DN 128:2978
TI Stable recombinant yeasts for fermenting **xylose** to **ethanol**
IN **Ho, Nancy W. Y.; Chen, Zheng-Dao**
PA Purdue Research Foundation, USA; Ho, Nancy W. Y.; Chen, Zheng-Dao
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N001-16
ICS C12N001-18; C12N001-19; C12N015-09; C12N015-68; C12N015-69;

C12N015-81; C12P007-06
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**

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FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI WO 9742307	A1	19971113	WO 1997-US7663	19970506	<--
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM					
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
AU 9728301	A1	19971126	AU 1997-28301	19970506	<--
AU 731102	B2	20010322			
EP 898616	A1	19990303	EP 1997-922698	19970506	<--
R: AT, BE, DE, DK, ES, FR, GB, GR, IT, NL, SE, PT, IE, FI					
CN 1225125	A	19990804	CN 1997-196195	19970506	<--
JP 2000509988	T2	20000808	JP 1997-540153	19970506	<--
BR 9710963	A	20010731	BR 1997-10963	19970506	<--
PRAI US 1996-16865P	P	19960506	<--		
WO 1997-US7663	W	19970506	<--		

AB Described are recombinant yeast which ferment **xylose** to **EtOH** and which maintain their ability to do so when cultured for numerous generations in non-selective media. The preferred yeast contain multiple copies of integrated genes encoding **xylose reductase**, **xylitol dehydrogenase**, and **xylulokinase** fused to promoters which are non-**glucose** inhibited and which do not require **xylose** for induction. Also described are preferred methods for integrating multiple copies of exogenous DNA into host cells by transforming cells with replicative/integrative vectors, and then replicating the cells a no. of times under selective pressure to promote retention of the vector in subsequent generations. The replicated vectors thus serve to integrate multiple copies of the exogenous DNA into the host cells throughout the replication/selection phase. Thereafter the selective pressure can be removed to promote loss of the vector in subsequent generations, leaving stable integrants of the exogenous DNA.

ST Saccharomyces recombinant **ethanol** fermn **xylose**

IT **Genetic engineering**
Saccharomyces cerevisiae
(stable recombinant yeasts for fermenting **xylose** to **ethanol**)

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(stable recombinant yeasts for fermenting **xylose** to **ethanol**)

IT **9028-16-4, Xylitol dehydrogenase**
9030-58-4, Xylulokinase 99775-25-4, Xylose reductase
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process); USES (Uses)
(stable recombinant yeasts for fermenting **xylose** to **ethanol**)

IT **58-86-6, D-Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(stable recombinant yeasts for fermenting **xylose** to

ethanol)
IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(stable recombinant yeasts for fermenting **xylose** to **ethanol**)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

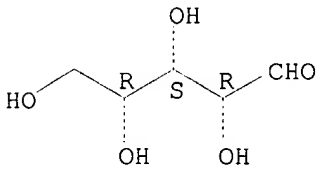
IT **9028-16-4**, **Xylitol dehydrogenase**
9030-58-4, **Xylulokinase** **99775-25-4**, **Xylose reductase**
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process); USES (Uses)
(stable recombinant yeasts for fermenting **xylose** to **ethanol**)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 9030-58-4 HCAPLUS
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 99775-25-4 HCAPLUS
CN Reductase, D-xylose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6**, **D-Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(stable recombinant yeasts for fermenting **xylose** to **ethanol**)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



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L70 ANSWER 4 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:589590 HCAPLUS
DN 127:258567
TI Expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization
AU Walfridsson, M.; Anderlund, M.; Bao, X.; Hahn-Hagerdal, B.
CS Department of Applied Microbiology, Lund Institute of Technology/Lund University, Lund, S-221, Swed.
SO Applied Microbiology and Biotechnology (**1997**), 48(2), 218-224

CODEN: AMBIDG; ISSN: 0175-7598
PB Springer
DT Journal
LA English
CC 3-4 (Biochemical **Genetics**)
Section cross-reference(s): 16

AB **Saccharomyces cerevisiae** was transformed with the Pichia stipitis CBS 6054 XYL1 and XYL2 genes encoding **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH) resp. The XYL1 and XYL2 genes were placed under the control of the alc. dehydrogenase 1 (ADH1) and phosphoglycerate kinase (PGK1) promoters in the yeast vector YEp24. Different vector constructions were made resulting in different specific activities of XR and XDH. The XR:XDH ratio (ratio of specific enzyme activities) of the transformed **S. cerevisiae** strains varied from 17.5 to 0.06. To enhance **xylose** utilization in the XYL1-, XYL2-contg. **S. cerevisiae** strains, the native genes encoding transketolase and transaldolase were also overexpressed. A strain with an XR:XDH ratio of 17.5 formed 0.82 g xylitol/g consumed **xylose**, whereas a strain with an XR:XDH ratio of 5.0 formed 0.58 g xylitol/g **xylose**. The strain with an XR:XDH ratio of 0.06, formed no xylitol and less glycerol and acetic acid compared with strains with the higher XR:XDH ratios. In addn., the strain with an XR:XDH ratio of 0.06 produced more **ethanol** than the other strains.

ST Pichia gene XYL1 XYL2 cloning Saccharomyces; **xylose reductase xylitol dehydrogenase** Pichia Saccharomyces

IT **Gene, microbial**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(XYL1; expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)

IT **Gene, microbial**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(XYL2; expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)

IT **Molecular cloning**
Saccharomyces cerevisiae
Yamadazyma stipitis
(expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)

IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)

IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)

IT 56-81-5, Glycerol, biological studies **64-17-5, Ethanol**, biological studies 64-19-7, Acetic acid, biological studies 87-99-0,

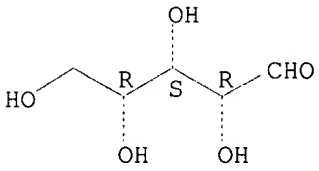
Xylitol
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(formation in **S. cerevisiae** strains contg. genes XYL1 and XYL2; expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)

IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **64-17-5, Ethanol**, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(formation in **S. cerevisiae** strains contg. genes XYL1 and XYL2; expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilization)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

L70 ANSWER 5 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:315590 HCAPLUS
DN 127:16516

TI Influence of cosubstrate concentration on **xylose** conversion by recombinant, XYL1-expressing **Saccharomyces cerevisiae**: a comparison of different sugars and **ethanol** as cosubstrates

AU Meinander, Nina Q.; Hahn-Hagerdal, Barbel
CS Dep. Applied Microbiol., Lund Inst. Techol./Univ. Lund, Lund, S-22 100, Swed.

bad date

SO Applied and Environmental Microbiology (**1997**), 63(5), 1959-1964
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
CC 16-2 (**Fermentation** and Bioindustrial Chemistry)
Section cross-reference(s): 10

AB Conversion of **xylose** to xylitol by recombinant **S. cerevisiae** expressing the XYL1 gene, encoding **xylose reductase**, was investigated by using different cosubstrates as generator of reduced cofactors. The effect of a pulse addn. of the cosubstrate on **xylose** conversion in cosubstrate-limited fed-batch cultivation was studied. **Glucose**, mannose, and fructose, which are transported with high affinity by the same transport system as is **xylose**, inhibited **xylose** conversion by 99, 77, and 78%, resp., reflecting competitive inhibition of **xylose** transport. Pulse addn. of maltose, which is transported by a specific transport system, did not inhibit **xylose** conversion. Pulse addn. of galactose, which is also transported by a specific transporter, inhibited **xylose** conversion by 51%, in accordance with noncompetitive inhibition between the galactose and **glucose**/**xylose** transport systems. Pulse addn. of **EtOH** inhibited **xylose** conversion by 15%, explained by inhibition of **xylose** transport through interference with the hydrophobic regions of the cell membrane. The xylitol yields on the different cosubstrates varied widely. Galactose gave the highest xylitol yield, 5.6-fold higher than that for **glucose**. The difference in redox metab. of **glucose** and galactose was suggested to enhance the availability of reduced cofactors for **xylose** redn. with galactose. The differences in xylitol yield obsd. between some of the other sugars may also reflect differences in redox metab. With all cosubstrates, the xylitol yield was higher under cosubstrate limitation than with cosubstrate excess.

ST xylitol prodn **xylose** Saccharomyces sugar cosubstrate; sugar metab Saccharomyces **xylose** redn xylitol; galactose metab Saccharomyces **xylose** redn xylitol

IT Metabolism, microbial
(redox; sugar and **ethanol** cosubstrate concn. effect on **xylose** conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

IT **Saccharomyces cerevisiae**
(sugar and **ethanol** cosubstrate concn. effect on **xylose** conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

IT **50-99-7**, **Glucose**, biological studies 57-48-7, D-Fructose, biological studies 59-23-4, D-Galactose, biological studies **64-17-5**, **Ethanol**, biological studies 69-79-4, Maltose 3458-28-4, D-Mannose
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(sugar and **ethanol** cosubstrate concn. effect on **xylose** conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

IT 87-99-0P, Xylitol
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(sugar and **ethanol** cosubstrate concn. effect on

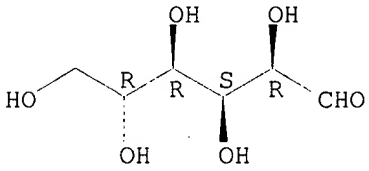
xylose conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

IT **58-86-6**, D-**Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(sugar and **ethanol** cosubstrate concn. effect on **xylose** conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

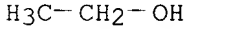
IT **50-99-7**, **Glucose**, biological studies **64-17-5**, **Ethanol**, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(sugar and **ethanol** cosubstrate concn. effect on **xylose** conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

RN 50-99-7 HCAPLUS
CN D-Glucose (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.



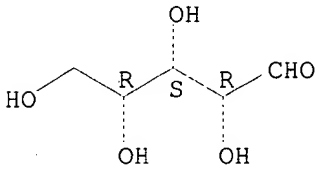
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)



IT **58-86-6**, D-**Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(sugar and **ethanol** cosubstrate concn. effect on **xylose** conversion to xylitol by recombinant XYL1-expressing **Saccharomyces cerevisiae**)

RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



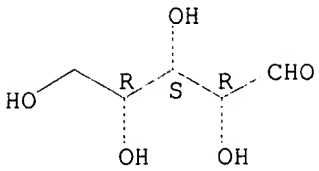
L70 ANSWER 6 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1997:208281 HCAPLUS
DN 126:198660
TI **Xylose-fermenting** microorganisms
AU Kordowska-Wiater, Monika; Targonski, Zdzislaw
CS Pol.
SO Postepy Mikrobiologii (**1996**), 35(3), 313-328
CODEN: PMKMAV; ISSN: 0079-4252

PB Polskie Towarzystwo Mikrobiologow
DT Journal; General Review
LA Polish
CC 17-0 (Food and Feed Chemistry)
AB A review with 77 refs. on the conversion of D-**xylose** into **ethanol** by **xylose fermenting** microorganisms that belong to different genera of yeasts, bacteria and mycelial fungi. Yeast such as Candida shehatae, C. tenuis, Pichia stipitis, P. segobiensis and Pachysolen tannophilus have been investigated; C. shehatae and P. stipitis were shown to produce over 20 g/L **ethanol**. On the other hand, bacteria from the certain species of Clostridium, Bacillus and Enterobacteriaceae have been described and were shown to posses certain advantages and disadvantages in relation to yeasts. These features include resp. short generation time and **fermn**. time, ability to **ferment** both pentose and hexose found in hemicellulosic materials and prodn. of excess byproducts. Fungi such as Fusarium, Mucor, Monila and Neurospora have been shown to **ferment** and produce low yields of **ethanol**. Novel methods directed to improving ethanolic yield by these microorganisms include mutation, protoplast fusion and recombinant techniques. These methods are led to isolation of species devoid of the ability to oxidize **ethanol**, flocculants and mutants with decreased **glucose** assimilation. In addn. cloning **xylose reductase** and **xylitol dehydrogenase** genes of P. stipitis and expressing them in yeast **S. cerevisiae** has been obtained. These methods creates the new possibilities of **xylose fermn**.
ST review **ethanol** prodn **xylose fermenting** microorganism
IT **Fermentation**
(**ethanol** with **xylose-fermenting** microorganisms)
IT Bacteria (Eubacteria)
Fungi
Yeast
(**xylose-fermenting** microorganisms)
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(prodn. with **xylose-fermenting** microorganisms)
IT **58-86-6, D-Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**xylose-fermenting** microorganisms).
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(prodn. with **xylose-fermenting** microorganisms)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **58-86-6, D-Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**xylose-fermenting** microorganisms)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 7 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1996:450313 HCAPLUS
DN 125:112897
TI Continuous **fermentation** by conventional and recombinant **Saccharomyces cerevisiae** immobilized in Ca-alginate beads hardened with trivalent ion
AU Roca, E.; Meinander, N.; Nunez, M. J.; Hahn-Hagerdal, B.; Lema, J. M.
CS Department Chemical Engineering Department, University Santiago de Compostela, Santiago de Compostela, E-15706, Spain
SO Progress in Biotechnology (**1996**), 11(Immobilized Cells), 173-180
CODEN: PBITE3; ISSN: 0921-0423
PB Elsevier
DT Journal
LA English
CC 16-9 (**Fermentation** and Bioindustrial Chemistry)
AB **Saccharomyces cerevisiae** is immobilized in trivalent ion (Al+3)-harden alginate beads. The effect of immobilization in cell retention and viability on the **ethanol** and xylitol manuf. in continuous reactor was studied. Also the plasmid stability and the evolution of **xylose reductase** activity in the recombinant yeast under anaerobic and O limitations was studied.
ST Saccharomyces immobilization calcium alginate trivalent ion
IT **Fermentation**
(alc.; continuous **fermn.** by conventional and recombinant **Saccharomyces cerevisiae** immobilized in Ca-alginate beads hardened with trivalent ion)
IT Immobilization, biochemical
Saccharomyces cerevisiae
(continuous **fermn.** by conventional and recombinant **Saccharomyces cerevisiae** immobilized in Ca-alginate beads hardened with trivalent ion)
IT 22537-23-1, Aluminum(3+), biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(continuous **fermn.** by conventional and recombinant **Saccharomyces cerevisiae** immobilized in Ca-alginate beads hardened with trivalent ion)
IT 9005-35-0, Calcium alginate
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(trivalent ion in hardening; continuous **fermn.** by conventional and recombinant **Saccharomyces cerevisiae** immobilized in Ca-alginate beads hardened with trivalent ion)

L70 ANSWER 8 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1996:308481 HCAPLUS
DN 124:340999
TI A metabolic engineering view on molecular breeding of an alcohol fermenting yeast from **xylose**
AU Seki, Tatsuji; Tantirungkij, Manee; Fujiyama, Kazuhito; Yoshida, Toshiomi
CS International Center Cooperative Research Biotechnology, Osaka University, Suita, 565, Japan
SO Environmental Biotechnology: Principles and Applications, [Papers presented at the International Symposium on Environmental Biotechnology],

Waterloo, Ont., July 4-8, 1994 (**1996**), Meeting Date 1994, 114-124. Editor(s): Moo-Young, Murray; Anderson, William A.; Chakrabarty, Ananda M. Publisher: Kluwer, Dordrecht, Neth.
CODEN: 62UGA4
DT Conference
LA English
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**

AB **Xylose**-assimilating **S. cerevisiae** was constructed by introducing the **xylose reductase** and **xylitol dehydrogenase** genes originating from P. stipitis. Good growth of the transformant in **xylose** medium was obsd. under aerobic conditions. Under a limited oxygen condition, the transformant produced a lesser amt. of **ethanol** than P. stipitis, and a remarkable amt. of xylitol was accumulated. A mutant, IM2, in which the ratio of **xylose reductase** to **xylitol dehydrogenase** activities was lower than the parental strain, exhibited an improved fermn. with less accumulation of xylitol and a higher yield. The limited feeding of **xylose** could also improve the fermn., with reduced xylitol accumulation as well as increased **ethanol** yield. The facts suggest strongly that the path of the conversion from xylitol to xylulose is the "bottleneck" due to a poor regeneration of NAD essential for the conversion. An appropriate oxygen supply also improved the **ethanol** prodn. and the prodn. rate, suggesting it may contribute to the NAD recycle from NADH.

ST **ethanol** manuf Saccharomyces **xylose**

IT Fermentation
Genetic engineering
Saccharomyces cerevisiae
(genetic engineering of yeast for **ethanol** fermn. from **xylose**)

IT **58-86-6, Xylose**, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(genetic engineering of yeast for **ethanol** fermn. from **xylose**)

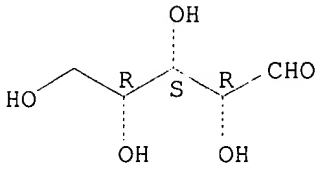
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(genetic engineering of yeast for **ethanol** fermn. from **xylose**)

IT 87-99-0P, Xylitol
RL: BYP (Byproduct); PREP (Preparation)
(genetic engineering of yeast for **ethanol** fermn. from **xylose**)

IT **58-86-6, Xylose**, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(genetic engineering of yeast for **ethanol** fermn. from **xylose**)

RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



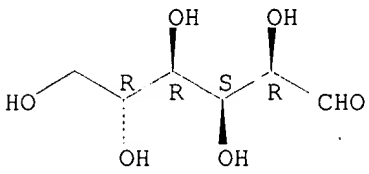
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(genetic engineering of yeast for **ethanol** fermn. from **xylose**)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

L70 ANSWER 9 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1996:278683 HCAPLUS
DN 124:315148
TI Xylulose and **glucose fermentation** by **Saccharomyces cerevisiae** in chemostat culture
AU Jeppsson, Helena; Yu, Shiyuan; Hahn-Haegerdal
CS Dep. Applied Microbiology, Lund Institute Technology/Univ. Lund, Lund, S-22100, Swed.
SO Applied and Environmental Microbiology (**1996**), 62(5), 1705-1709
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
CC 16-9 (**Fermentation** and Bioindustrial Chemistry)
AB **Saccharomyces cerevisiae** ATCC 24860 was cultivated in chemostat culture under anoxic conditions with 111.1 mmol of **glucose** liter-1 alone or with a mixt. of 66.7 mmol of xylulose liter-1 and 111.1 mmol of **glucose** liter-1. The substrate consumption rate was 5.4 mmol g of cells-1 h-1 for **glucose**, whereas for xylulose it was 1.0 mmol g of cells-1 h-1. The **ethanol** yield decreased from 0.52 carbon mole of **ethanol** produced per carbon mole of sugar consumed during the utilization of **glucose** alone to 0.49 carbon mole produced per carbon mole consumed during the simultaneous utilization of xylulose and **glucose**, while cell biomass was maintained at 2.04 to 2.10 g liter-1. Xylulose coutilization was accompanied by a shift in product formation from **ethanol** to acetate and arabinitrol. **Xylulokinase** activity was absent during **glucose** metab. but detectable during simultaneous utilization of xylulose and **glucose**. Xylulose cometabolism resulted in increased in vitro activity of pyruvate decarboxylase and an increased concn. of the intracellular metabolite fructose 1,6-diphosphate without significant changes in the concns. of 6-phosphogluconate and pyruvate. The results are discussed in relation to (i) altered enzyme activities and (ii) the redox flux of the cell.
ST xylulose **glucose** utilization Saccharomyces chemostat culture
IT **Fermentation**
Saccharomyces cerevisiae
(xylulose and **glucose fermn.** by **Saccharomyces cerevisiae** in chemostat culture)
IT 551-84-8P, Xylulose
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process)
(xylulose and **glucose fermn.** by **Saccharomyces cerevisiae** in chemostat culture)
IT **50-99-7, Glucose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(xylulose and **glucose fermn.** by

Saccharomyces cerevisiae in chemostat culture)
IT **50-99-7, Glucose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(xylulose and **glucose fermn.** by
Saccharomyces cerevisiae in chemostat culture)
RN 50-99-7 HCAPLUS
CN D-Glucose (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.

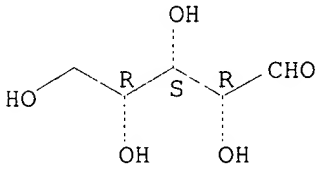


L70 ANSWER 10 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1996:55764 HCAPLUS
DN 124:111997
TI A heterologous reductase affects the redox balance of recombinant **Saccharomyces cerevisiae**
AU Meinander, Nina; Zacchi, Guido; Hahn-Haegerdal, Baerbel
CS Applied Microbiology, Chem. Eng., Lund Inst. Technology, Univ. Lund, Lund, S-22100, Swed.
SO Microbiology (Reading, United Kingdom) (**1996**), 142(1), 165-72
CODEN: MROBEO; ISSN: 1350-0872
PB Society for General Microbiology
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
AB Recombinant **Saccharomyces cerevisiae** harboring the **xylose reductase** (XR) gene XYL1 from Pichia stipitis was grown in anoxic chemostat culture at two different diln. rates. At each diln. rate a transient expt., encompassing a shift in the sugar content of the medium from **glucose** to **glucose** plus **xylose** , was performed. The steady states at the beginning and the end of the transients were compared in terms of specific product fluxes from **glucose** metab. At both diln. rates, the specific glycerol flux decreased and the specific acetate and CO2 fluxes increased. The specific **ethanol** flux was not affected. At the lower diln. rate, the prodn. of biomass decreased during the transient, but at the higher diln. rate it increased. The changes in product pattern can be explained as being due to the redox perturbation caused by the consumption of reduced cofactors in the XR-catalyzed reaction. Regeneration of NAD partly through **xylose** redn. instead of glycerol prodn. decreased the formation of glycerol. Addnl., **xylose** redn. activated those pathways which produce reduced cofactors, such as acetate formation and the pentose phosphate pathway, indicated by increased acetate and CO2 prodn. The dual cofactor specificity of XR, with a preference for NADPH over NADh, was evident from the effects of **xylose** redn. on product fluxes. Comparison of the **xylose** redn. rates at low and high **glucose** flux indicated that the supply of reduced cofactors partly controlled the reaction rate. At the higher diln. rate, control by some other factor such as **xylose** transport or XR activity increased. Calcn. of carbon balances at the steady states showed that all substrate carbon was recovered in biomass or products. Based on the specific product fluxes, calcns. of quant. cofactor balances at the steady states was attempted. However, sensitivity calcns. showed that anal. errors in the range of 5% caused substantial errors in the cofactor

balance, without affecting the carbon balance.
ST **xylose reductase** Saccharomyces carbon metab
IT Carbon metabolic pathway
Glycolysis
Molecular cloning
Pentose phosphate pathway
Saccharomyces cerevisiae
(heterologous **xylose reductase** affects redox balance of recombinant **Saccharomyces cerevisiae**)
IT **99775-25-4, Xylose reductase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(heterologous **xylose reductase** affects redox balance of recombinant **Saccharomyces cerevisiae**)
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(heterologous **xylose reductase** affects redox balance of recombinant **Saccharomyces cerevisiae**)
IT 87-99-0, Xylitol
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(heterologous **xylose reductase** affects redox balance of recombinant **Saccharomyces cerevisiae**)
IT **99775-25-4, Xylose reductase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(heterologous **xylose reductase** affects redox balance of recombinant **Saccharomyces cerevisiae**)
RN 99775-25-4 HCAPLUS
CN Reductase, D-xylose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(heterologous **xylose reductase** affects redox balance of recombinant **Saccharomyces cerevisiae**)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 11 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1995:974520 HCAPLUS
DN 124:4758
TI **Xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing the TKL1 and TAL1 genes encoding the pentose phosphate pathway enzymes transketolase and transaldolase
AU Walfridsson, Mats; Hallborn, Johan; Penttilae, Merja; Keraenen, Sirkka; Hahn-Haegerdal, Baerbel
CS Department of Applied Microbiology, Lund University, Lund, S-221 00, Swed.
SO Applied and Environmental Microbiology (**1995**), 61(12), 4184-90
CODEN: AEMIDF; ISSN: 0099-2240

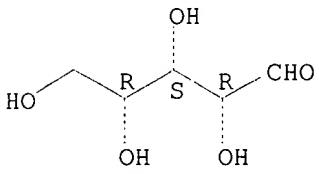
PB American Society for Microbiology
DT Journal
LA English
CC 10-4 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): **16**
AB **Saccharomyces cerevisiae** was metabolically engineered for **xylose** utilization. The Pichia stipitis CBS 6054 genes XYL1 and XYL2 encoding **xylose reductase** and **xylitol dehydrogenase** were cloned into **S. cerevisiae**. The gene products catalyze the two initial steps in **xylose** utilization which **S. cerevisiae** lacks. To increase the flux through the pentose phosphate pathway, the **S. cerevisiae** TKL1 and TAL1 genes encoding transketolase and transaldolase were overexpressed. A XYL1- and XYL2-contg. **S. cerevisiae** strain overexpressing TAL1 (S104-TAL) showed considerably enhanced growth on **xylose** compared with a strain contg. only XYL1 and XYL2. Overexpression of only TKL1 did not influence growth. The results indicate that the transaldolase level in **S. cerevisiae** is insufficient for the efficient utilization of pentose phosphate pathway metabolites. Mixts. of **xylose** and **glucose** were simultaneously consumed with the recombinant strain S104-TAL. The rate of **xylose** consumption was higher in the presence of **glucose**. **Xylose** was used for growth and xylitol formation, but not for **ethanol** prodn. Decreased oxygenation resulted in impaired growth and increased xylitol formation. **Fermn.** with strain S103-TAL, having a **xylose reductase/xylitol dehydrogenase** ratio of 0.5:30 compared with 4.2:5.8 for S104-TAL, did not prevent xylitol formation.
ST **xylose** utilization recombinant Saccharomyces
IT **Fermentation**
Pichia stipitis
Saccharomyces cerevisiae
(**xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing TKL1 and TAL1 genes encoding pentose phosphate pathway enzymes transketolase and transaldolase)
IT 9014-46-4, Transaldolase 9014-48-6, Transketolase **9028-16-4**, **Xylitol dehydrogenase 99775-25-4**, **Xylose reductase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(**xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing TKL1 and TAL1 genes encoding pentose phosphate pathway enzymes transketolase and transaldolase)
IT 87-99-0, Xylitol
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(**xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing TKL1 and TAL1 genes encoding pentose phosphate pathway enzymes transketolase and transaldolase)
IT **58-86-6**, **Xylose**, reactions
RL: RCT (Reactant); RACT (Reactant or reagent)
(**xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing TKL1 and TAL1 genes encoding pentose phosphate pathway enzymes transketolase and transaldolase)
IT **9028-16-4**, **Xylitol dehydrogenase 99775-25-4**, **Xylose reductase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(**xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing TKL1 and TAL1 genes encoding pentose phosphate pathway enzymes transketolase and transaldolase)
RN 9028-16-4 HCAPLUS

CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 99775-25-4 HCAPLUS
CN Reductase, D-xylose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6, Xylose**, reactions
RL: RCT (Reactant); RACT (Reactant or reagent)
(**xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing TKL1 and TAL1 genes encoding pentose phosphate pathway enzymes transketolase and transaldolase)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 12 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1995:756362 HCAPLUS
DN 123:196764
TI Recombinant yeasts for effective fermentation of **glucose** and **xylose**
IN **Ho, Nancy W. Y.**; Tsao, George T.
PA Purdue Research Foundation, USA
SO PCT Int. Appl., 62 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N001-14
ICS C12N009-00; C12N009-12; C12N015-00; C12P007-08
CC 16-5 (Fermentation and Bioindustrial Chemistry)
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9513362	A1	19950518	WO 1994-US12861	19941108	<--
	W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TJ, TT, UA, UZ, VN					
	RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
	US 5789210	A	19980804	US 1993-148581	19931108	<--
	CA 2176038	AA	19950518	CA 1994-2176038	19941108	<--
	AU 9510517	A1	19950529	AU 1995-10517	19941108	<--
	AU 695930	B2	19980827			
	EP 728192	A1	19960828	EP 1995-901176	19941108	<--
	R: AT, BE, DE, DK, ES, FR, GB, GR, IE, IT, NL, SE					
	BR 9408010	A	19961217	BR 1994-8010	19941108	<--
	CN 1141057	A	19970122	CN 1994-194767	19941108	<--
	JP 09505469	T2	19970603	JP 1994-513948	19941108	<--
	PL 176399	B1	19990531	PL 1994-314297	19941108	<--
	FI 9601926	A	19960704	FI 1996-1926	19960507	<--
PRAI	US 1993-148581	A	19931108	<--		
	US 1993-148541	A	19931108	<--		

WO 1994-US12861 W 19941108 <--

AB Described are recombinant yeasts contg. genes encoding **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase**, and DNA mols., vectors and methods useful for producing such yeasts. The recombinant yeasts effectively ferment **xylose** to **EtOH**, and preferred yeasts are capable of simultaneously fermenting **glucose** and **xylose** to **EtOH**, thereby taking full advantage of these 2 sugar sources as they are found in agricultural biomass.

ST recombinant yeast **ethanol** fermn **glucose xylose**

IT **Deoxyribonucleic acid sequences**
(for **xylulokinase** gene of **Saccharomyces cerevisiae**)

IT **Protein sequences**
(for **xylulokinase** of **Saccharomyces cerevisiae**)

IT Fermentation
Saccharomyces cerevisiae
(recombinant yeasts for effective fermn. of **glucose** and **xylose**)

IT **Gene, microbial**
RL: PRP (Properties)
(**xylulokinase**; sequence of **xylulokinase** gene of **Saccharomyces cerevisiae**)

IT **167078-89-9**
RL: PRP (Properties)
(amino acid sequence; recombinant yeasts for effective fermn. of **glucose** and **xylose**)

IT **167974-35-8**
RL: PRP (Properties)
(nucleotide sequence; recombinant yeasts for effective fermn. of **glucose** and **xylose**)

IT **9028-16-4, Xylitol dehydrogenase**
9030-58-4, Xylulokinase 99775-25-4, Xylose reductase
RL: CAT (Catalyst use); USES (Uses)
(recombinant yeasts contg. cloned enzyme genes for effective fermn. of **glucose** and **xylose**)

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(recombinant yeasts for effective fermn. of **glucose** and **xylose**)

IT **50-99-7, Glucose**, biological studies **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(recombinant yeasts for effective fermn. of **glucose** and **xylose**)

IT **167078-89-9**
RL: PRP (Properties)
(amino acid sequence; recombinant yeasts for effective fermn. of **glucose** and **xylose**)

RN 167078-89-9 HCAPLUS

CN Xylulokinase (Saccharomyces cerevisiae strain 1400 clone pLNH33 reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **167974-35-8**
RL: PRP (Properties)
(nucleotide sequence; recombinant yeasts for effective fermn. of **glucose** and **xylose**)

RN 167974-35-8 HCAPLUS
CN DNA (Saccharoymces cerevisiae strain 1400 clone pLNH33 xylulokinase gene plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **9028-16-4, Xylitol dehydrogenase**
9030-58-4, Xylulokinase 99775-25-4,
Xylose reductase
RL: CAT (Catalyst use); USES (Uses)
(recombinant yeasts contg. cloned enzyme genes for effective fermn. of **glucose** and **xylose**)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 9030-58-4 HCAPLUS
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)

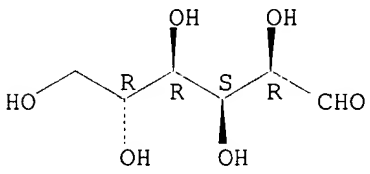
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 99775-25-4 HCAPLUS
CN Reductase, D-xylose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(recombinant yeasts for effective fermn. of **glucose** and **xylose**)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

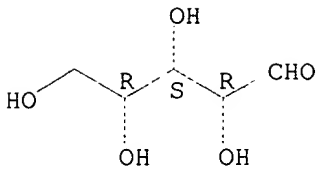
IT **50-99-7, Glucose**, biological studies **58-86-6,**
Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(recombinant yeasts for effective fermn. of **glucose** and **xylose**)
RN 50-99-7 HCAPLUS
CN D-Glucose (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.



RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 13 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1995:558793 HCAPLUS
DN 122:310445
TI Xylitol formation and reduction equivalent generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene
AU Thestrup, Helle Norgaard; Hahn-Haegerdal, Baerbel
CS Lund Institute Technology, Lund University, Lund, S-221 00, Swed.
SO Applied and Environmental Microbiology (**1995**), 61(5), 2043-5
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
AB **Glucose** was used as a cosubstrate under anaerobic conditions in the conversion of **xylose** to xylitol by a recombinant **Saccharomyces cerevisiae** strain expressing the xyl1 gene. **Glucose** was metabolized mainly through glycolysis, with carbon dioxide, acetate, and **ethanol** as end products and with redn. equiv. generated in the glyceraldehyde-3-phosphate dehydrogenase and acetaldehyde dehydrogenase reactions. At a high **glucose** supply rate, generation of surplus redn. equiv. resulted in simultaneous **ethanol** formation. On the other hand, at a low **glucose** supply rate, addnl. redn. equiv. were generated by simultaneous **ethanol** consumption. A significantly lower xylitol formation rate was obsd.
ST xylitol formation **xylose glucose** cosubstrate Saccharomyces; reducing equiv generation xylitol formation Saccharomyces; reductase **xylose** recombinant Saccharomyces xylitol formation
IT Glycolysis
Saccharomyces cerevisiae
(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)
IT **Gene, microbial**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(XYL1, for **xylose reductase**; xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)
IT **95829-40-6, Xylose reductase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(gene xyl1-encoded; xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)
IT 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase 37353-37-0, Acetaldehyde dehydrogenase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)

(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)

IT **50-99-7, Glucose**, biological studies **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)

IT **64-17-5, Ethanol**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)

IT 64-19-7, Acetic acid, biological studies 87-99-0, Xylitol 124-38-9, Carbon dioxide, biological studies
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)

IT **95829-40-6, Xylose reductase**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(gene xyl1-encoded; xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)

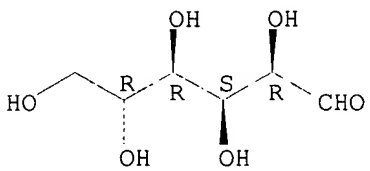
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **50-99-7, Glucose**, biological studies **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)

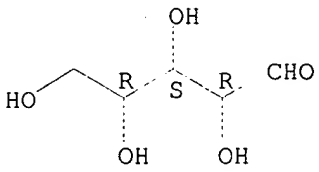
RN 50-99-7 HCAPLUS
CN D-Glucose (8CI, 9CI) (CA INDEX NAME)

Absolute stereochemistry.



RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **64-17-5**, **Ethanol**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(xylitol formation and redn. equiv. generation during anaerobic **xylose** conversion with **glucose** as cosubstrate in recombinant **Saccharomyces cerevisiae** expressing the xyl1 gene)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

L70 ANSWER 14 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1995:396765 HCAPLUS
DN 122:158719
TI Fed-batch xylitol production with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate
AU Meinander, N.; Hahn-Haegerdal, B.; Linko, M.; Linko, P.; Ojamo, H.
CS VTT, Biotechnical Laboratory, Espoo, SF-02151, Finland
SO Applied Microbiology and Biotechnology (**1994**), 42(2-3), 334-9
CODEN: AMBIDG; ISSN: 0175-7598
PB Springer
DT Journal
LA English
CC 16-5 (**Fermentation** and Bioindustrial Chemistry)
AB The bioconversion of **xylose** into xylitol in fed-batch **fermn.** with a recombinant **Saccharomyces cerevisiae** strain, transformed with the **xylose-reductase** gene of Pichia stipitis, was studied. When only **xylose** was fed into the **fermentor**, the prodn. of xylitol continued until the **ethanol** that had been produced during an initial growth phase on **glucose**, was depleted. It was concluded that **ethanol** acted as a redox-balance-retaining co-substrate. The conversion of high amts. of **xylose** into xylitol required the addn. of **ethanol** to the feed soln. Under O2-limited conditions, acetic acid accumulated in the **fermn.** broth, causing poisoning of the yeast at low extracellular pH. Acetic acid toxicity could be avoided by either increasing the pH from 4,5 to 6.5 or by more effective aeration, leading to the further metab. of acetic acid into cell mass. The best xylitol/**ethanol** yield, 2.4 g g-1 was achieved under O2-limited conditions. Under anaerobic conditions **ethanol** could not be used as a co-substrate, because the cell cannot produce ATP for maintenance requirements from **ethanol** anaerobically. The specific rate of xylitol prodn. decreased with increasing aeration. The initial volumetric productivity increased when **xylose** was added in portions rather than by continuous feeding, due to a more complete satn. of the transport system and the **xylose reductase**

enzyme.
ST xylitol **fermn** recombinant Saccharomyces **ethanol** cosubstrate
IT **Saccharomyces cerevisiae**
(fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
IT **Fermentation**
(fed-batch, fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
IT **95829-40-6, Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Pichia stipitis gene for; fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
IT 87-99-0P, Xylitol
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
IT **64-17-5, Ethanol**, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
IT **95829-40-6, Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Pichia stipitis gene for; fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **64-17-5, Ethanol**, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(fed-batch xylitol prodn. with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

L70 ANSWER 15 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1995:221244 HCAPLUS
DN 122:8066
TI Yeast **xylose** metabolism and xylitol production
AU Ojamo, Heikki
CS VTT Biotechnology and Food Research, Finland
SO VTT Publications (**1994**), 176, 91pp.
CODEN: VTTPEY; ISSN: 1235-0621
DT Journal
LA English
CC 16-5 (**Fermentation** and Bioindustrial Chemistry)
Section cross-reference(s): 10
AB A screening method was used for testing yeast strains in shake flask

cultivations for their ability to convert **xylose** to xylitol. Of the 37 different strains studied, by far the best were Candida guilliermondii C-6, C. tropicalis C-86 and C. tropicalis C-87. Of these strains, C-6 was superior in a tech. sense, being able to convert **xylose** to xylitol with a yield of 0.5 g g-1 at **xylose** concns. at least up to 300 g L-1, whereas the other two strains did not tolerate **xylose** concns. more than 120 g L-1. **Fermn.** kinetics in **xylose** conversion were studied more closely with the strain C-6 both in shake flasks and in a **fermenter**. Oxygen availability was the key process variable. In order to quantify its effect on yeast metab., oxygen transfer characteristics for both shake flasks and a **fermenter** were detd. The rate of specific **xylose** uptake by the yeast was independent of the oxygen transfer rate above a certain threshold value. The growth of the yeast could be limited by oxygen limitation, under which conditions a typical overflow metab. resulted in very efficient xylitol prodn. Under optimum conditions for oxygen transfer, the yield of xylitol from **xylose** was 0.74 g g-1 and the rate of specific xylitol prodn. was about 0.22 g g-1h-1. An initial **xylose** concn. of 200 g L-1 slowed down the **xylose** conversion, but this effect could be avoided by a fed-batch **fermn.**, in which the **xylose** concn. was controlled to 40-50 g L-1. By this method the process time was decreased by 40 % and the yield of xylitol was increased from 0.6 to 0.78 g g-1 compared with a batch **fermn.** The metab. of xylitol could also be limited by addn. of the glycolytic and TCA-cycle inhibitor furfuraldehyde at a concn. of 0.6 mL L-1 under which conditions the limitation by oxygen was less crit. for xylitol prodn. **Xylose** metab. was studied both by cultivation expts. and by simulation of a structured math. model. The model was constructed on the basis of the assumption of pseudo-steady-state of intracellular NADH, NADPH and ATP concns. The basis for xylitol accumulation appeared to be the high efficiency of the oxidative pentose phosphate cycle. This was verified by **fermn.** results, according to which the value of the RQ rose up to 10. The values of the activities or the affinities of the first two enzymes in **xylose** metab., **xylose reductase** and **xylitol dehydrogenase**, could not explain xylitol accumulation. The activity of **xylitol dehydrogenase** was four to sixfold compared with that of **xylose reductase**, and the Km value of **xylitol dehydrogenase** for xylitol was not higher than 60 mM. **Xylose reductase** was strictly specific for NADPH and **xylitol dehydrogenase** for NAD, which both favor xylitol accumulation under oxygen limitation. The structured math. model of **xylose** metab. in the strain C-6 was combined to a model describing the performance of the **fermenter**. On the basis of the simulation using this combined model the **fermn.** could be optimized in relation to, e.g., oxygen transfer. Xylitol prodn. was also studied with a genetically modified **Saccharomyces cerevisiae** strain carrying a gene coding for **xylose reductase** in a vector under the constitutive **S. cerevisiae** PGK-promoter. By feeding this strain with a cosubstrate and **xylose** under carefully controlled conditions of dissolved oxygen concn., yields of xylitol from **xylose** of over 0.95 g g-1 were achieved. **Ethanol** was used as the cosubstrate to regenerate the cofactor and for cell maintenance. The molar yield of xylitol on **ethanol** at the optimum dissolved oxygen concn. was about 1 mol mol-1. Thus, about half of the reducing power produced from **ethanol** was used for the redn. of **xylose**. **Glucose** inhibited **xylose** uptake very efficiently and was therefore not a suitable cosubstrate.

ST yeast **xylose** metab xylitol manuf

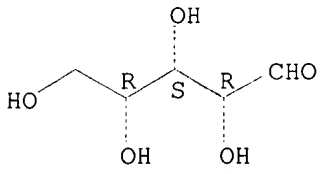
IT Simulation and Modeling, biological
(of yeast **xylose** metab. and xylitol prodn.)

IT Candida
Fermentation
(yeast **xylose** metab. and xylitol prodn.)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(in yeast **xylose** metab. and xylitol prodn.)
IT 87-99-0P, Xylitol
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(yeast **xylose** metab. and xylitol prodn.)
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(yeast **xylose** metab. and xylitol prodn.)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(in yeast **xylose** metab. and xylitol prodn.)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(yeast **xylose** metab. and xylitol prodn.)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 16 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1994:653726 HCAPLUS
DN 121:253726
TI Biochemistry and physiology of **xylose fermentation** by yeasts
AU Hahn-Haegerdal, B.; Jeppsson, H.; Skoog, K.; Prior, B. A.
CS Dep. Appl. Microbiology, Lund Inst. Technology, Lund, Swed.
SO Enzyme and Microbial Technology (**1994**), 16(11), 933-43
CODEN: EMTED2; ISSN: 0141-0229
DT Journal; General Review
LA English
CC 16-0 (**Fermentation** and Bioindustrial Chemistry)
AB A review with 103 refs. The rate of **ethanol** prodn. and the **ethanol** concns. attained by the most promising **xylose-fermenting** yeasts, Pichia stipitis, Candida shehatae, and

Pachysolen tannophilus, compare poorly with that of com. **ethanol fermn.** by non-**xylose-fermenting** **Saccharomyces cerevisiae** using **glucose**-based substrates. The oxygen requirement for efficient **fermn.** by the **xylose-fermenting** yeasts and the lack of such a general requirement by **S. cerevisiae** indicates basic underlying differences in their physiol. relations to oxygen. The redox imbalance in the initial conversion of **xylose** to xylulose, sensitivity to high concns. of **ethanol**, differences in the respiratory pathway and sensitivity to microbial inhibitors, particularly those liberated during pretreatment and hydrolysis of lignocellulose substrates, have been identified as major factors limiting **ethanol fermn.** by the **xylose-fermenting** yeasts. Recombinant **S. cerevisiae**, contg. functional **xylose reductase** and **xylitol** **dehydrogenase**, grows on, but poorly **ferments**, **xylose**. The unfavorable kinetic properties of these enzymes and an inadequate pentose phosphate pathway apparently limit the ability of the recombinant yeast to **ferment xylose**.

ST review **ethanol fermn xylose** yeast

IT **Fermentation**
Yeast
(biochem. and physiol. of **xylose fermn.** by yeasts)

IT **64-17-5P, Ethanol**, biological studies
RL: BMF (Bioindustrial manufacture); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(biochem. and physiol. of **xylose fermn.** by yeasts)

IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(biochem. and physiol. of **xylose fermn.** by yeasts)

IT **64-17-5P, Ethanol**, biological studies
RL: BMF (Bioindustrial manufacture); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(biochem. and physiol. of **xylose fermn.** by yeasts)

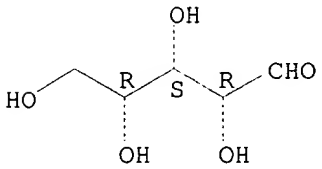
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(biochem. and physiol. of **xylose fermn.** by yeasts)

RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



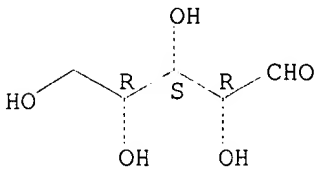
L70 ANSWER 17 OF 28 HCAPLUS COPYRIGHT 2003 ACS

AN 1994:653725 HCAPLUS
DN 121:253725
TI Strain selection, taxonomy, and genetics of **xylose-fermenting** yeasts
AU Jeffries, T. W.; Kurtzman, C. P.
CS Forest Products Lab., US Dep. Agriculture, Madison, WI, USA
SO Enzyme and Microbial Technology (**1994**), 16(11), 922-32
CODEN: EMTED2; ISSN: 0141-0229
DT Journal; General Review
LA English
CC 16-0 (**Fermentation** and Bioindustrial Chemistry)
AB A review with 103 refs. The objective of this review is to trace the development of **xylose-fermenting** yeast strains from their discovery in 1980. Following initial reports, screens of known yeasts identified five species of interest: Candida shehatae, Candida tenuis, Pachysolen tannophilus, Pichia segobiensis, and Pichia stipitis. Candida shehatae strains can be divided into three varieties. Pachysolen tannophilus and Pichia stipitis have been studied most extensively and have the best-understood genetic systems. Improved mutants of P. tannophilus have been obtained by selecting for an inability to oxidize **ethanol** and for rapid growth on xylitol and nitrate. Improved P. stipitis mutants have been obtained by selecting for flocculation, decreased utilization of **glucose**, and growth on noninductive carbon sources. Bacterial **xylose** isomerase has been cloned and expressed in **S. cerevisiae** and Schizosaccharomyces pombe, but the heterologous enzyme is inactive. **Xylose reductase** and **xylitol dehydrogenase** have been cloned from P. stipitis and expressed in **Saccharomyces cerevisiae**, giving rise to transformant **S. cerevisiae** that grow on **xylose** but that **ferment** it poorly. A transformation and expression system based on the URA3 marker has recently been developed for P. stipitis so that contemporary genetic methods may be brought to bear on this organism.
ST review **xylose fermenting** yeast genetic selection
IT **Fermentation**
Genetic selection
Taxonomy
Yeast
(strain selection, taxonomy, and genetics of **xylose-fermenting** yeasts)
IT **64-17-5P, Ethanol**, biological studies
RL: BMF (Bioindustrial manufacture); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(strain selection, taxonomy, and genetics of **xylose-fermenting** yeasts)
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(strain selection, taxonomy, and genetics of **xylose-fermenting** yeasts)
IT **64-17-5P, Ethanol**, biological studies
RL: BMF (Bioindustrial manufacture); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PREP (Preparation)
(strain selection, taxonomy, and genetics of **xylose-fermenting** yeasts)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **58-86-6**, **Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(strain selection, taxonomy, and genetics of **xylose-fermenting** yeasts)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

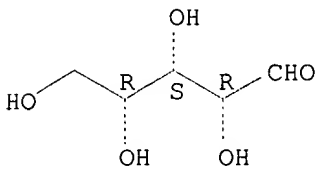
Absolute stereochemistry.



L70 ANSWER 18 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1994:650854 HCAPLUS
DN 121:250854
TI Bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**
AU Carlsen, Helle N.; Hallborn, Johan; Gorwa, Marie-Francoise; Hahn-Haegerdal, Baerbel
CS Chemical Center, University Lund, Lund, S-221 00, Swed.
SO Progress in Biotechnology (**1994**), 9(ECB6: PROCEEDINGS OF THE 6TH EUROPEAN CONGRESS ON BIOTECHNOLOGY, 1993, PT. 1), 313-16
CODEN: PBITE3; ISSN: 0921-0423
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): **3**
AB The **xylose reductase** gene of Pichia stipitis was cloned into **S. cerevisiae**. The recombinant **S. cerevisiae** was thus able to convert **xylose** to xylitol. The cofactor NAD(P)H, used for **xylose** redn., could be generated in situ through the oxidn. of **ethanol**, acetate, or **glucose**.
ST **xylose** metab Saccharomyces recombinant
IT **Molecular cloning**
Saccharomyces cerevisiae
(bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**)
IT **58-86-6**, **Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**)
IT **53-57-6**, NADPH **58-68-4**, NADH
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**)
IT 87-99-0, Xylitol
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**)
IT **58-86-6**, **Xylose**, biological studies

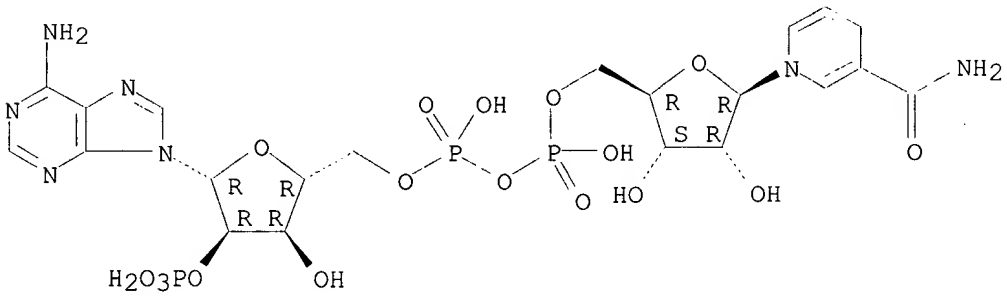
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **53-57-6**, NADPH **58-68-4**, NADH
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(bioconversion of **xylose** to xylitol with in situ generation of NAD(P)H in recombinant **Saccharomyces cerevisiae**)
RN 53-57-6 HCAPLUS
CN Adenosine 5'-(trihydrogen diphosphate), 2'-(dihydrogen phosphate), P'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosyl-3-pyridinecarboxamide (9CI) (CA INDEX NAME)

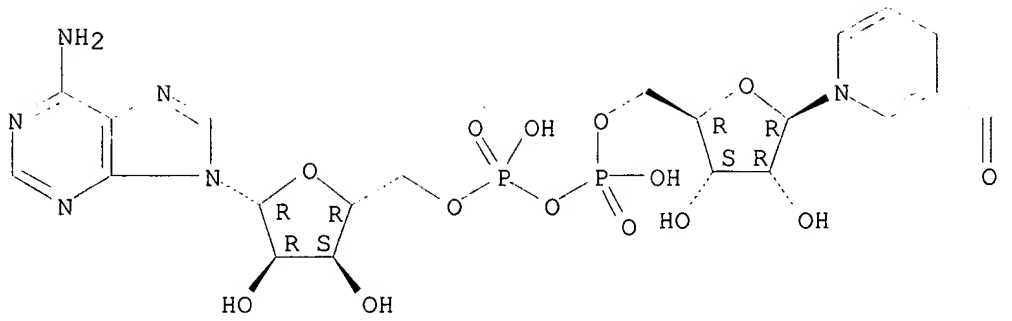
Absolute stereochemistry.



RN 58-68-4 HCAPLUS
CN Adenosine 5'-(trihydrogen diphosphate), P'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosyl-3-pyridinecarboxamide (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A

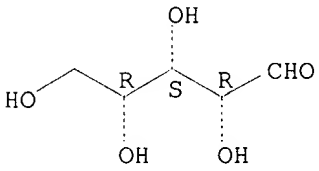


PAGE 1-B

L70 ANSWER 19 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1994:433237 HCAPLUS
DN 121:33237
TI Fed-batch **fermentation** of **xylose** by a fast-growing mutant of **xylose**-assimilating recombinant **Saccharomyces cerevisiae**
AU Tantirungkij, Manee; Izuishi, Tamaki; Seki, Tatsuji; Yoshida, Toshiomi
CS Fac. Eng., Osaka Univ., Suita, 565, Japan
SO Applied Microbiology and Biotechnology (**1994**), 41(1), 8-12
CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
CC 16-5 (**Fermentation** and Bioindustrial Chemistry)
Section cross-reference(s): 10
AB Mutants of **xylose**-assimilating recombinant **Saccharomyces cerevisiae** carrying the **xylose reductase** and **xylitol dehydrogenase** genes on plasmid pEXGD8 were selected, after Et methanesulfonate treatment, for their rapid growth on **xylose** medium. The fastest growing strain (strain IM2) showed a lower activity of **xylose reductase** but a higher ratio of **xylitol dehydrogenase** to **xylose reductase** activities than the parent strain, as well as high **xylulokinase** activity. Southern hybridization of the chromosomal DNA indicated that plasmid pEXGD8 was integrated into the chromosome of mutant IM2, resulting in an increase in the stability of the cloned genes. In batch **fermn**. under O2 limitation, the yield and prodn. rate of **ethanol** were improved 1.6 and 2.7 times, resp., compared to the parent strain. In fed-batch culture with slow feeding of **xylose** and appropriate O2 supply at a low level, xylitol excreted from the cells was limited and the **ethanol** yield increased 1.5 times over that in the batch culture, with a high initial concn. of **xylose**, although the prodn. rate was reduced. The results suggested that slow conversion of **xylose** to xylitol led to a lower level of intracellular xylitol, resulting in less excretion of xylitol, and an increase in the **ethanol** yield. It was also obsd. that the oxidn. of xylitol was strongly affected by the O2 supply.
ST recombinant Saccharomyces **ethanol fermn xylose**

; genetic selection yeast **ethanol fermn xylose**
IT Genetic selection
(of recombinant **Saccharomyces cerevisiae**, for **ethanol fermn.** of **xylose**)
IT **Saccharomyces cerevisiae**
(recombinant, **ethanol fermn.** of **xylose** by)
IT **Fermentation**
(fed-batch, **ethanol**, from **xylose** by recombinant **Saccharomyces cerevisiae**)
IT **58-86-6**, D-**Xylose**, biological studies
RL: BIOL (Biological study)
(**ethanol** prodn. from, by recombinant **Saccharomyces cerevisiae**)
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manuf. of, from **xylose** by recombinant **Saccharomyces cerevisiae**)
IT **9028-16-4**, NAD-dependent **Xylitol dehydrogenase**
9030-58-4, Xylulokinase 95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(of recombinant **Saccharomyces cerevisiae**, **ethanol fermn.** of **xylose** in relation to)
IT **58-86-6**, D-**Xylose**, biological studies
RL: BIOL (Biological study)
(**ethanol** prodn. from, by recombinant **Saccharomyces cerevisiae**)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manuf. of, from **xylose** by recombinant **Saccharomyces cerevisiae**)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **9028-16-4**, NAD-dependent **Xylitol dehydrogenase**
9030-58-4, Xylulokinase 95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(of recombinant **Saccharomyces cerevisiae**, **ethanol fermn.** of **xylose** in relation to)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 9030-58-4 HCAPLUS
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L70 ANSWER 20 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1993:404708 HCAPLUS
DN 119:4708
TI **Xylose fermentation** by **Saccharomyces cerevisiae**
AU Koetter, Peter; Ciriacy, Michael
CS Inst. Mikrobiol., Heinrich-Heine-Univ., Duesseldorf, W-4000/1, Germany
SO Applied Microbiology and Biotechnology (**1993**), 38(6), 776-83
CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
AB The authors performed a comparative study of **xylose** utilization in **Saccharomyces cerevisiae** transformants expressing two key enzymes in **xylose** metab., **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH), and in a prototypic **xylose**-utilizing yeast, Pichia stipitis. In the absence of respiration, baker's yeast cells convert half of the **xylose** to xylitol and **ethanol**, whereas P. stipitis cells display a homofermentative conversion of **xylose** to **ethanol**. Xylitol prodn. by baker's yeast is interpreted as a result of the dual cofactor dependence of the XR and the generation of NADPH by the pentose phosphate pathway. Further limitations of **xylose** utilization in **S. cerevisiae** cells are probably caused by an insufficient capacity of the nonoxidative pentose phosphate pathway, as indicated by accumulation of sedoheptulose-7-phosphate and the absence of fructose-1,6-bisphosphate and pyruvate accumulation. By contrast, uptake at high substrate concns. probably does not limit **xylose** conversion in **S. cerevisiae** XYL1/XYL2 transformants.
ST **xylose fermn** Saccharomyces
IT Biological transport
(of **xylose**, by **Saccharomyces cerevisiae**)
IT Pichia stipitis
Saccharomyces cerevisiae
(**xylose** metab. by)
IT **64-17-5, Ethanol**, biological studies 87-99-0, Xylitol
RL: FORM (Formation, nonpreparative)
(formation of, from **xylose** by **Saccharomyces cerevisiae**)
IT **9028-16-4 95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(in **Saccharomyces cerevisiae, xylose** metab. in relation to)
IT **58-86-6, D-Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of, by **Saccharomyces cerevisiae**)
IT **64-17-5, Ethanol**, biological studies
RL: FORM (Formation, nonpreparative)
(formation of, from **xylose** by **Saccharomyces cerevisiae**)

RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

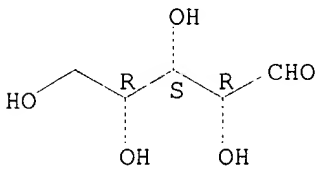
H_3C-CH_2-OH

IT **9028-16-4 95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(in **Saccharomyces cerevisiae, xylose** metab. in relation to)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **58-86-6, D-Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of, by **Saccharomyces cerevisiae**)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 21 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1993:226769 HCAPLUS
DN 118:226769
TI Isolation of **xylose reductase** gene of Pichia stipitis and its expression in **Saccharomyces cerevisiae**
AU Takuma, Shinya; Nakashima, Noriyuki; Tantirungkij, Manee; Kinoshita, Shinichi; Okada, Hirosuke; Seki, Tatsuji; Yoshida, Toshiomi
CS Fac. Eng., Osaka Univ., Suita, 565, Japan
SO Applied Biochemistry and Biotechnology (**1991**), 28-29, 327-40
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal
LA English
CC 3-2 (Biochemical **Genetics**)
Section cross-reference(s): 7, 10
AB A NADPH/NADH-dependent **xylose reductase** gene was isolated from the **xylose**-assimilating yeast, Pichia stipits. DNA sequence anal. showed that the gene consists of 951 bp. The gene introduced in **Saccharomyces cerevisiae** was transcribed to mRNA, and a considerable amt. of enzyme activity was obsd. constitutively, whereas transcription and translation in P. stipitis were inducible. **S. cerevisiae** carrying the **xylose reductase** gene could not, however, grow on **xylose** medium, and could not produce **ethanol** from **xylose**. Since **xylose** uptake and accumulation of xylitol by **S. cerevisiae** were obsd., the conversion of xylitol to xylulose

seemed to be limited.
ST Pichia **xylose reductase** gene cloning sequence; Saccharomyces cloning **xylose reductase** gene Pichia
IT **Saccharomyces cerevisiae**
(cloning and expression in, of **xylose reductase** gene, of Pichia stipitis)
IT **Gene, microbial**
RL: BIOL (Biological study)
(for **xylose reductase**, of Pichia stipitis, cloning and expression and sequencing of)
IT **Deoxyribonucleic acid sequences**
(of **xylose reductase** gene, of Pichia stipitis)
IT **Molecular cloning**
(of **xylose reductase** gene, of Pichia stipitis, for expression in yeast)
IT **Protein sequences**
(of **xylose reductase**, of Pichia stipitis)
IT Pichia stipitis
(**xylose reductase** gene of, sequence and expression in yeast of)
IT **138263-97-5**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)
IT **95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(gene for, of Pichia stipitis, cloning and expression and sequencing of)
IT 147651-00-1
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)
IT **138263-97-5**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)
RN 138263-97-5 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (Yamadazyma stipitis clone pUA103 gene XYL1 precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(gene for, of Pichia stipitis, cloning and expression and sequencing of)
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L70 ANSWER 22 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1993:190040 HCAPLUS
DN 118:190040
TI Secretion of a xylanase from Cryptococcus albidus by **Saccharomyces cerevisiae** and Pichia stipitis
AU Morosoli, Rolf; Zalce, Eugenia; Moreau, Alain; Durand, Serge
CS Cent. Rech. Microbiol. Appl., Inst. Armand-Frappier, Ville de Laval, QC, H7N 4Z3, Can.
SO Progress in Biotechnology (**1992**), 7(Xylans Xylanases), 247-58
CODEN: PBITE3; ISSN: 0921-0423
DT Journal
LA English

CC 16-4 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): 3
AB The xylanase gene of Cryptococcus albidus and its cDNA were each inserted in the vector pVT100 and in the vector pJHS to transform **Saccharomyces cerevisiae** and Pichia stipitis, resp. The xylanase gene was under the control of its own promoter for expts. in **S. cerevisiae**, while in P. stipitis it was under the control of the **xylose reductase** promoter of the same strain. Yeasts transformed with plasmids contg. the cDNA of the structural xylanase gene produced active extracellular xylanase. The enzyme secreted by **S. cerevisiae** had an apparent mol. mass of 48-kDa, which corresponds to that of the native xylanase produced by C. albidus. The enzyme synthesized by P. stipitis, however, had an apparent mol. mass of 50-kDa, probably reflecting a different protein glycosylation level by this strain. With plasmids bearing the genomic xylanase gene, transcription occurred, but the seven introns interrupting the xylanase gene were neither spliced out by **S. cerevisiae** nor by P. stipitis and no enzyme was produced. Expression of the xylanase gene by P. stipitis, resulted in a yeast able to grow on xylan as carbon source, directly fermenting it to **ethanol** under anaerobic conditions.
ST Cryptococcus xylanase gene cloning Saccharomyces Pichia
IT Pichia stipitis
Saccharomyces cerevisiae
(cloning and expression in, of xylanase gene of Cryptococcus albidus)
IT **Gene, microbial**
RL: BIOL (Biological study)
(for xylanase, of Streptococcus albidus, cloning and expression in **Saccharomyces cerevisiae** and Pichia stipitis of)
IT **Molecular cloning**
(of xylanase gene, of Cryptococcus albidus, in **Saccharomyces cerevisiae** and Pichia stipitis)
IT Cryptococcus albidus
(xylanase gene of, cloning and expression of, in **Saccharomyces cerevisiae** and Pichia stipitis)
IT 37278-89-0, Xylanase
RL: BIOL (Biological study)
(gene for, of Cryptococcus albidus, cloning and expression in **Saccharomyces cerevisiae** and Pichia stipitis of)

L70 ANSWER 23 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1993:167538 HCAPLUS
DN 118:167538
TI Construction of **xylose**-assimilating **Saccharomyces cerevisiae**
AU Tantirungkij, Manee; Nakashima, Noriyuki; Seki, Tatsuji; Yoshida, Toshiomi
CS Fac. Eng., Osaka Univ., Suita, 565, Japan
SO Journal of Fermentation and Bioengineering (**1993**), 75(2), 83-8
CODEN: JFBIEX; ISSN: 0922-338X
DT Journal
LA English
CC 16-5 (Fermentation and Bioindustrial Chemistry)
AB The **xylose reductase** gene originating from Pichia stipitis was subcloned on an expression vector with the enolase promoter and terminator from **S. cerevisiae**. The transformants of **S. cerevisiae** harboring the resultant plasmids produced **xylose reductase** constitutively at a rate .apprx.3-fold higher than P. stipitis, but could not assimilate **xylose** due to the deficient conversion of xylitol to xylulose. The **xylitol dehydrogenase** gene was also isolated from the gene library of P. stipitis by plaque hybridization using a probe specific for its N-terminal amino acid sequence. The gene transferred into **S. cerevisiae** was well expressed. High

expressions of the **xylose reductase** and **xylitol dehydrogenase** genes in **S. cerevisiae** were achieved by introducing both genes on the same or coexisting plasmids. The transformants grew on a medium contg. **xylose** as the sole C source, but **EtOH** prodn. from **xylose** was less than that by P. stipitis and a significant amt. of xylitol was excreted into the culture broth.

ST **xylose** fermn Saccharomyces genetic engineering; **ethanol** fermn **xylose** recombinant Saccharomyces; Pichia **xylose** metab gene Saccharomyces; reductase **xylose** Pichia Saccharomyces; **xylitol dehydrogenase** Pichia Saccharomyces

IT **Gene, microbial**
RL: BIOL (Biological study)
(for **xylose reductase** and **xylitol dehydrogenase**, of Pichia stipitis, construction of **Saccharomyces cerevisiae** contg.)

IT **Genetic engineering**
(of **Saccharomyces cerevisiae**, for **xylose** fermn.)

IT **Saccharomyces cerevisiae**
(**xylose**-fermenting, construction of)

IT Pichia stipitis
(**xylose**-metabolizing enzymes of, construction of **Saccharomyces cerevisiae** contg.)

IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(fermn. of, construction of **Saccharomyces cerevisiae** for)

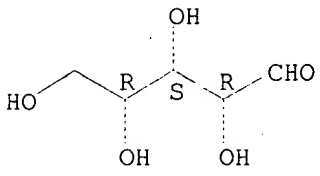
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manuf. of, from **xylose**, recombinant **Saccharomyces cerevisiae** for)

IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(of Pichia stipitis, **xylose** fermn. by **Saccharomyces cerevisiae** contg.)

IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(fermn. of, construction of **Saccharomyces cerevisiae** for)

RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manuf. of, from **xylose**, recombinant **Saccharomyces cerevisiae** for)

RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(of Pichia stipitis, **xylose** fermn. by **Saccharomyces cerevisiae** contg.)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L70 ANSWER 24 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1992:406110 HCAPLUS
DN 117:6110
TI Isolation and characterization of acetic acid-tolerant galactose-**fermenting** strains of **Saccharomyces cerevisiae** from a spent sulfite liquor **fermentation** plant
AU Linden, Torbjoern; Peetre, Johan; Hahn-Haegerdal, Baerbel
CS Chem. Cent., Lund Univ., Lund, S-221 00, Swed.
SO Applied and Environmental Microbiology (**1992**), 58(5), 1661-9
CODEN: AEMIDF; ISSN: 0099-2240
DT Journal
LA English
CC 16-9 (**Fermentation** and Bioindustrial Chemistry)
Section cross-reference(s): 10
AB From a continuous spent sulfite liquor **fermn.** plant, two species of yeast were isolated, Saccharomcyes cerevisiae and Pichia membranaefaciens. One of the isolates of **S. cerevisiae**, no. 3, was heavily flocculating and produced a higher **ethanol** yield from spent sulfite liquor than did com. bakers' yeast. The greatest difference between isolate 3 and bakers' yeast was that of galactose **fermn.**, even when galactose utilization was induced, i.e., when they were grown in the presence of galactose, prior to **fermn.** Without acetic acid present, both bakers' yeast and isolate 3 **fermented glucose** and galactose sequentially. Galactose **fermn.** with bakers' yeast was strongly inhibited by acetic acid at pH values below 6. Isolate 3 **fermented** galactose, **glucose**, and mannose without catabolite repression in the presence of acetic acid, even at pH 4.5. The **xylose reductase** (EC 1.1.1.21) and **xylitol dehydrogenase** (EC 1.1.1.9) activities were detd. in some of the isolates as well as in two strains of **S. cerevisiae** (ATCC 24860 and bakers' yeast) and Pichia stipitis CBS 6054. The **S. cerevisiae** strains manifested **xylose reductase** activity that was 2 orders of magnitude less than the corresponding P. stipitis value of 890 nmol/min/mg protein. The **xylose** dehydrogenase activity was 1 order of magnitude less than the corresponding activity of P. stipitis (330 nmol/min/mg protein).
ST spent sulfite liquor acetate tolerant Saccharomyces; galactose metab acetate yeast **xylose reductase**
IT Pichia membranaefaciens
Saccharomyces cerevisiae
(acetic acid-tolerant galactose-**fermenting**, from spent sulfite liquor, isolation and characterization of)
IT Pulping liquors, biological studies

RL: BIOL (Biological study)
(sulfite, spent, acetic acid-tolerant galactose-**fermenting** **Saccharomyces cerevisiae** from, isolation and characterization of)
IT 59-23-4, Galactose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of, by acetic acid-tolerant **Saccharomyces cerevisiae** from spent sulfite liquor)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(of acetic acid-tolerant galactose-**fermenting** **Saccharomyces cerevisiae**, from spent sulfite liquor)
IT 7782-99-2
RL: BIOL (Biological study)
(pulping liquors, sulfite, spent, acetic acid-tolerant galactose-**fermenting Saccharomyces cerevisiae** from, isolation and characterization of)
IT 64-19-7, Acetic acid, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(tolerance to, of galactose-**fermenting Saccharomyces cerevisiae** from spent sulfite liquor **fermn**. plant)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(of acetic acid-tolerant galactose-**fermenting** **Saccharomyces cerevisiae**, from spent sulfite liquor)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L70 ANSWER 25 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1992:52957 HCAPLUS
DN 116:52957
TI Cloning of yeast **xylose reductase** and **xylitol dehydrogenase** genes and their use
IN Strasser, Alexander W. M.; Hollenberg, Cornelis P.; Von Ciriacy-Wantrup, Michael; Koetter, Peter; Amore, Rene; Piontek, Michael; Hagedorn, Jutta
PA Rhein Biotech Gesellschaft fuer neue Biotechnologische Prozesse und Produkte m.b.H., Germany
SO Ger. Offen., 51 pp.
CODEN: GWXXBX
DT Patent
LA German
IC ICM C12N001-19
ICS C12N015-63; C12P019-34; C07H021-04; C07K015-04
CC 3-4 (Biochemical **Genetics**)
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI DE 4009676	A1	19911002	DE 1990-4009676	19900326 <--
DE 4009676	C2	19930909		
EP 450430	A2	19911009	EP 1991-104558	19910322 <--
EP 450430	A3	19920102		
EP 450430	B1	19970625		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE

	AT 154829	E	19970715	AT 1991-104558	19910322	<--
	ES 2104626	T3	19971016	ES 1991-104558	19910322	<--
	CA 2039021	AA	19910927	CA 1991-2039021	19910325	<--
	JP 06339383	A2	19941213	JP 1991-62160	19910326	<--
	JP 3122153	B2	20010109			
	JP 2000139486	A2	20000523	JP 2000-589	19910326	<--
	JP 2001103988	A2	20010417	JP 2000-276227	19910326	<--
	JP 3193917	B2	20010730			
PRAI	DE 1990-4009676	A	19900326	<--		
	JP 1991-62160	A3	19910326	<--		

AB The XYL1 gene encoding **xylose reductase** and the XYL2 gene encoding **xylitol dehydrogenase** of Pichia stipitis are cloned, sequenced, and expressed in other microorganisms. Yeast transformants expressing these genes can be used to prep. **EtOH**, alc. beverages, or biomass. The promoters of these genes can be used to express genes in yeast. A **Saccharomyces cerevisiae** mutant contg. both genes was prepd. and used to prep. **EtOH** in .apprx.80% yield from **xylose**. Plasmids contg. Clostridium thermocellum cellulase gene linked to the promoter of XYL1 or XYL2 were prepd. and P. stipitis transformed with them. These transformants produced the enzyme in response to **xylose** induction.

ST XYL1 XYL2 gene Pichia cloning; **xylose reductase** gene Pichia; **xylitol dehydrogenase** gene Pichia; Saccharomyces transformant **ethanol** manuf **xylose**

IT Fermentation
(alc., yeast expressing XYL1 and/or XYL2 genes of Pichia stipitis for)

IT Paecilomyces
Saccharomyces cerevisiae
Schizosaccharomyces
Schizosaccharomyces pombe
Zymomonas
(expression in, of XYL1 and XYL2 genes of Pichia stipitis)

IT **Protein sequences**
(of **xylitol dehydrogenase** of Pichia stipitis, complete)

IT **Protein sequences**
(of **xylose reductase** of Pichia stipitis, complete)

IT **Molecular cloning**
(of XYL1 and XYL2 genes of Pichia stipitis, in yeast)

IT **Plasmid and Episome**
(pMPGC1-2, cellulase gene of Clostridium on, expression in Pichia stipitis of)

IT **Plasmid and Episome**
(pR2, **xylose reductase** gene XYL1 of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pXDH, **xylitol dehydrogenase** gene XYL2 fragment of Pichia stipitis on)

IT **Plasmid and Episome**
(pXDH-HIS3, **xylitol dehydrogenase** gene XYL2 of Pichia stipitis on, expression in Schizosaccharomyces pombe of)

IT **Plasmid and Episome**
(pXR, **xylose reductase** gene XYL1 of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pXR-LEU2, **xylose reductase** gene XYL1 of Pichia stipitis on, expression in Schizosaccharomyces pombe of)

IT **Plasmid and Episome**
(pXRa, **xylose reductase** gene, XYL1 fragment of Pichia stipitis on)

IT **Plasmid and Episome**
(pXRb, **xylose reductase** gene XYL1 fragment of

Pichia stipitis on)
IT Biomass
(prepn. of, yeast expressing XYL1 and/or XYL2 genes of Pichia stipitis for)
IT **Deoxyribonucleic acid sequences**
(**xylitol dehydrogenase**-specifying, of Pichia stipitis, complete)
IT Candida
Debaryomyces
Hansenula
Kluyveromyces
Metschnikowia
Pachysolen (fungus)
Pichia
Saccharomyces
Schwanniomyces
(**xylose reductase** and **xylitol dehydrogenase** genes of, cloning of, cloning of XYL1 and XYL2 genes of Pichia stipitis in relation to)
IT **Deoxyribonucleic acid sequences**
(**xylose reductase**-specifying, of Pichia stipitis, complete)
IT Pichia stipitis
(XYL1 and XYL2 genes of, cloning and expression in yeast of)
IT **Plasmid and Episome**
(pD1, **xylitol dehydrogenase** gene XYL2 of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)
IT **Plasmid and Episome**
(pD2, **xylitol dehydrogenase** gene XYL2 of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)
IT **Plasmid and Episome**
(pR1, **xylose reductase** gene XYL1 of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)
IT **Plasmid and Episome**
(pRD1, **xylose reductase** gene XYL1 and **xylitol dehydrogenase** gene XYL2 of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)
IT **Genetic element**
RL: BIOL (Biological study)
(promoter, of XYL1 and XYL2 genes of Pichia stipitis, heterologous gene expression in yeast using)
IT **Gene, microbial**
RL: BIOL (Biological study)
(XYL1, cloning and expression of, of Pichia stipitis, in yeast)
IT **Gene, microbial**
RL: BIOL (Biological study)
(XYL2, cloning and expression of, of Pichia stipitis, in yeast)
IT 136511-83-6 **138263-97-5**
RL: BIOL (Biological study)
(amino acid sequence of and expression in Saccharomyces of gene for)
IT 136510-54-8, Deoxyribonucleic acid (Pichia stipitis clone pD1 gene XYL2) 136510-55-9, Deoxyribonucleic acid (Pichia stipitis clone pD1 gene XYL2 plus 5'- and 3'-flanking region fragment) 138575-98-1, Deoxyribonucleic acid (Pichia stipitis clone pR1 gene XYL1) 138575-99-2, Deoxyribonucleic acid (Pichia stipitis clone pR1 gene XYL1 plus 5'- and 3'-flanking region fragment)
RL: BIOL (Biological study)
(cloning and expression in Saccharomyces and nucleotide sequence of)
IT 138575-97-0, Deoxyribonucleic acid (Pichia stipitis clone pD1 gene XYL2 promoter region-containing fragment) 138576-00-8, Deoxyribonucleic acid (Pichia stipitis clone pR1 gene XYL1 promoter region-containing fragment)

RL: PRP (Properties)
(gene expression in yeast using and nucleotide sequence of)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(gene for, of Pichia stipitis, cloning and expression in yeast of)
IT **64-17-5P, Ethanol**, preparation
RL: PREP (Preparation)
(manuf. of, yeast transformants expressing XYL1 and XYL2 genes of Pichia stipitis for)
IT **53-57-6P**, NADPH **53-59-8P**, NADP+
RL: PREP (Preparation)
(prepn. of, from NADPH, **xylose reductase** of Pichia stipitis for)
IT 551-84-8, Xylulose
RL: BIOL (Biological study)
(yeast mutants growing on, XYL1 and XYL2 genes of Pichia stipitis expression in and enzyme manuf. with)
IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(yeast transformed with XYL1 and/or XYL2 genes of Pichia growth on, for biomass prepn.)
IT **138263-97-5**
RL: BIOL (Biological study)
(amino acid sequence of and expression in Saccharomyces of gene for)
RN 138263-97-5 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (Yamadazyma stipitis clone pUA103 gene XYL1 precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(gene for, of Pichia stipitis, cloning and expression in yeast of)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

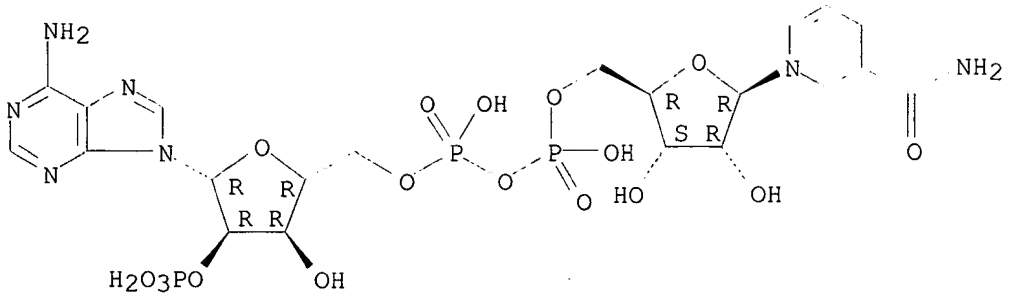
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **64-17-5P, Ethanol**, preparation
RL: PREP (Preparation)
(manuf. of, yeast transformants expressing XYL1 and XYL2 genes of Pichia stipitis for)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **53-57-6P**, NADPH **53-59-8P**, NADP+
RL: PREP (Preparation)
(prepn. of, from NADPH, **xylose reductase** of Pichia stipitis for)
RN 53-57-6 HCAPLUS
CN Adenósine 5'-(trihydrogen diphosphate), 2'-(dihydrogen phosphate), P'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosyl-3-pyridinecarboxamide (9CI) (CA INDEX NAME)

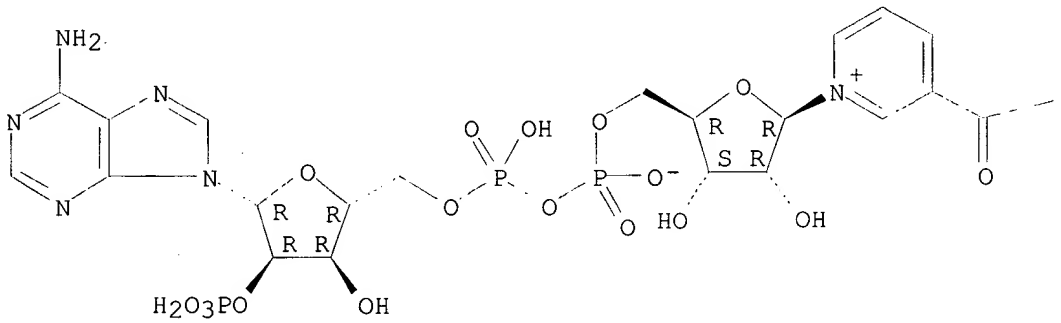
Absolute stereochemistry.



RN 53-59-8 HCAPLUS
CN Adenosine 5'-(trihydrogen diphosphate), 2'-(dihydrogen phosphate), P'.fwdarw.5'-ester with 3-(aminocarbonyl)-1-.beta.-D-ribofuranosylpyridinium, inner salt (9CI) (CA INDEX NAME)

Absolute stereochemistry.

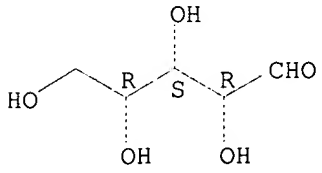
PAGE 1-A



PAGE 1-B

IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(yeast transformed with XYL1 and/or XYL2 genes of Pichia growth on, for biomass prepn.)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



L70 ANSWER 26 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1992:35663 HCAPLUS
DN 116:35663
TI Recombinant yeasts containing DNA sequences coding for **xylose reductase** and **xylitol dehydrogenase**
IN Hallborn, Johan; Penttila, Merja; Ojamo, Heikki; Walfridsson, Mats; Airaksinen, Ulla; Keranen, Sirkka; Hahn-Hagerdal, Barbel
PA Valtion Teknillinen Tutkimuskeskus, Finland
SO PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-53
ICS C12N009-04
CC 3-4 (Biochemical **Genetics**)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9115588	A1	19911017	WO 1991-FI103	19910408	<--
	W: AU, CA, FI, JP, NO, US					
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE					
	FI 9001771	A	19911007	FI 1990-1771	19900406	<--
	CA 2090122	AA	19911007	CA 1991-2090122	19910408	<--
	AU 9175657	A1	19911030	AU 1991-75657	19910408	<--
	AU 647104	B2	19940317			
	EP 527758	A1	19930224	EP 1991-906996	19910408	<--
	EP 527758	B1	19980107			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE					
	JP 05507843	T2	19931111	JP 1991-506907	19910408	<--
	JP 3348215	B2	20021120			
	AT 161886	E	19980115	AT 1991-906996	19910408	<--
	ES 2113373	T3	19980501	ES 1991-906996	19910408	<--
	NO 9203880	A	19921006	NO 1992-3880	19921006	<--
	US 5866382	A	19990202	US 1994-336198	19941103	<--
	FI 9902153	A	19991006	FI 1999-2153	19991006	<--
PRAI	FI 1990-1771	A	19900406	<--		
	US 1990-527775	A2	19900524	<--		
	WO 1991-FI103	A	19910408	<--		
	US 1992-848694	B1	19920309	<--		
	FI 1992-4461	A	19921002	<--		

AB A cDNA for yeast **xylose reductase** is cloned and sequenced. This cDNA is expressed in recombinant yeast, optionally along with that for **xylitol dehydrogenase**. These recombinant yeast can be used to prep. xylitol, or **ethanol** (when both genes are expressed), from **xylose** or **xylose** -contg. materials. The **xylose reductase** cDNA of Pichia stipitis was cloned. **Saccharomyces cerevisiae** transformants expressing this cDNA were used to prep. xylitol. **S. cerevisiae** expressing both **xylose reductase** and **xylitol dehydrogenase** produced **EtOH**, xylitol, and biomass from spent sulfite liquor.
ST **xylose reductase** cDNA Pichia cloning; xylitol **ethanol** manuf recombinant Saccharomyces
IT **Gene, microbial**
RL: BIOL (Biological study)
(cDNA, for **xylose reductase** of Pichia stipitis, cloning and expression in **Saccharomyces cerevisiae** of)
IT Kluyveromyces
Pichia
Saccharomyces cerevisiae

Schizosaccharomyces pombe
Yeast
(expression in, of **xylose reductase** cDNA of Pichia stipitis)

IT **Molecular cloning**
(of **xylose reductase** cDNA of Pichia stipitis, in **Saccharomyces cerevisiae**)

IT **Protein sequences**
(of **xylose reductase** of Pichia stipitis, complete)

IT **Plasmid and Episome**
(pJHXDH60, **xylitol dehydrogenase** cDNA of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pJHXDH70, **xylitol dehydrogenase** cDNA of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pJHXR22, **xylose reductase** cDNA of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pMW22, **xylitol dehydrogenase** cDNA of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pUA103, **xylose reductase** cDNA of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT **Plasmid and Episome**
(pUA107, **xylose reductase** cDNA of Pichia stipitis on, expression in **Saccharomyces cerevisiae** of)

IT Pichia stipitis
(**xylose reductase** cDNA of, cloning and expression in **Saccharomyces cerevisiae** of)

IT **Deoxyribonucleic acid sequences**
(**xylose reductase**-specifying, of Pichia stipitis, complete)

IT **138263-97-5**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of and cloning of cDNA for)

IT **95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(cDNA for, of Pichia stipitis, cloning and expression in **Saccharomyces cerevisiae** of)

IT **9028-16-4, Xylitol dehydrogenase**
RL: BIOL (Biological study)
(cDNA for, recombinant yeast expressing **xylose reductase** cDNA and, **ethanol** manuf. with)

IT 138263-60-2, Deoxyribonucleic acid (Pichia stipitis clone pUA103 gene xrd minus terminator fragment)
RL: PRP (Properties); BIOL (Biological study)
(cloning and nucleotide sequence of)

IT 87-99-0P, Xylitol
RL: PREP (Preparation)
(manuf. of, from **xylose**, recombinant yeast **xylose reductase** for)

IT **64-17-5P, Ethanol**, preparation
RL: PREP (Preparation)
(manuf. of, recombinant yeast expressing **xylose reductase** and **xylitol dehydrogenase** cDNAs for)

IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(xylitol manuf. from, recombinant yeast expressing cloned

xylose reductase cDNA for)
IT **138263-97-5**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of and cloning of cDNA for)
RN 138263-97-5 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (Yamadazyma stipitis clone pUA103 gene XYL1 precursor reduced) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(cDNA for, of Pichia stipitis, cloning and expression in **Saccharomyces cerevisiae** of)
RN 95829-40-6 HCAPLUS
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)

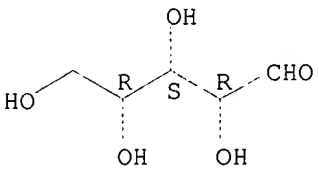
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **9028-16-4, Xylitol dehydrogenase**
RL: BIOL (Biological study)
(cDNA for, recombinant yeast expressing **xylose reductase** cDNA and, **ethanol** manuf. with)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **64-17-5P, Ethanol**, preparation
RL: PREP (Preparation)
(manuf. of, recombinant yeast expressing **xylose reductase** and **xylitol dehydrogenase** cDNAs for)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(xylitol manuf. from, recombinant yeast expressing cloned **xylose reductase** cDNA for)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

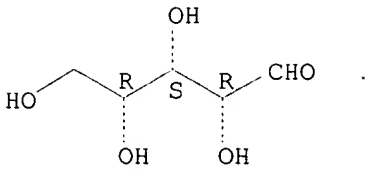
Absolute stereochemistry.



L70 ANSWER 27 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN 1990:422145 HCAPLUS
DN 113:22145
TI **Xylulokinase** activity in various yeasts including **Saccharomyces cerevisiae** containing the cloned **xylulokinase** gene

AU Deng, Xue Xing; **Ho, Nancy W. Y.**
CS A. A. Potter Eng. Cent., Purdue Univ., West Lafayette, IN, 47907, USA
SO Applied Biochemistry and Biotechnology (**1990**), 24-25, 193-9
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal
LA English
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**, 10
AB D-**Xylose** is a major constituent of hemicellulose, which makes up 20-30% of the renewable biomass in nature. D-**Xylose** can be fermented by most yeasts, including **S. cerevisiae**, by a 2-stage process. In this process, **xylose** is 1st converted to xylulose in vitro by **xylose** (**glucose**) isomerase, and the latter sugar is then fermented by yeast to **EtOH**. With the availability of an inexpensive source of **xylose** isomerase produced by recombinant Escherichia coli, this process of fermenting **xylose** to **EtOH** can become quite effective. Yeast **xylose** and xylulose fermn. was further improved by cloning and overexpression of the **xylulokinase** gene. For instance, the level of **xylulokinase** activity in **S. cerevisiae** was increased 230-fold by cloning its **xylulokinase** gene on a high copy-no. plasmid, coupled with fusion of the gene with an effective promoter. The resulting genetically engineered yeasts can ferment **xylose** and xylulose more than twice as fast as the parent yeast.
ST **xylulokinase** gene cloning yeast **ethanol** fermn; Saccharomyces xylulose fermn **xylulokinase** gene
IT Fermentation
(**ethanol**, from **xylose** by yeast, **xylulokinase** gene cloning in)
IT **Gene and Genetic element, microbial**
RL: PROC (Process)
(for **xylulokinase**, cloning of, in yeast for **ethanol** fermn.)
IT **Molecular cloning**
(of **xylulokinase** gene, in yeast for **ethanol** fermn.)
IT Yeast
(**xylulokinase** activities in)
IT **Saccharomyces cerevisiae**
(**xylulokinase** gene cloning in, for **ethanol** fermn.)
IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(**ethanol** fermn. of, by yeast, **xylulokinase** gene cloning in)
IT **9030-58-4, Xylulokinase**
RL: BIOL (Biological study)
(gene for, cloning of, in yeast for **ethanol** fermn.)
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manuf. of, from **xylose** by yeast, **xylulokinase** gene cloning in)
IT **58-86-6, Xylose**, biological studies
RL: BIOL (Biological study)
(**ethanol** fermn. of, by yeast, **xylulokinase** gene cloning in)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **9030-58-4, Xylulokinase**
RL: BIOL (Biological study)
(gene for, cloning of, in yeast for **ethanol** fermn.)
RN 9030-58-4 HCAPLUS
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)

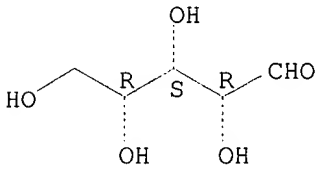
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manuf. of, from **xylose** by yeast, **xylulokinase** gene cloning in)
RN 64-17-5 HCAPLUS
CN Ethanol (9CI) (CA INDEX NAME)

H_3C-CH_2-OH

L70 ANSWER 28 OF 28 HCAPLUS COPYRIGHT 2003 ACS
AN **1986:403229** HCAPLUS
DN **105:3229**
TI Direct evidence for a **xylose** metabolic pathway in **Saccharomyces cerevisiae**
AU Batt, C. A.; Carvallo, S.; Easson, D. D., Jr.; Akedo, M.; Sinskey, A. J.
CS Dep. Appl. Biol. Sci., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA
SO Biotechnology and Bioengineering (**1986**), 28(4), 549-53
CODEN: BIBIAU; ISSN: 0006-3592
DT Journal
LA English
CC 10-2 (Microbial Biochemistry)
AB **Xylose** transport, **xylose reductase**, and **xylitol dehydrogenase** activities are demonstrated in **S. cerevisiae**. The enzymes in the **xylose** catabolic pathway necessary for the conversion of **xylose** to xylulose are present, although **S. cerevisiae** cannot grow on **xylose** as a sole C source. **Xylose** transport is less efficient than **glucose** transport, and its rate is dependent upon aeration. **Xylose reductase** appears to be a **xylose**-inducible enzyme and **xylitol dehydrogenase** activity is constitutive, although both are repressed by **glucose**. Both **xylose reductase** and **xylitol dehydrogenase** activities are 5-10-fold lower in **S. cerevisiae** as compared to Candida utiliz. In vivo conversion of [14C]**xylose** in **S. cerevisiae** is demonstrated and xylitol is detected, although no significant levels of any other 14C-labeled metabolites (e.g., **EtOH**) are obsd.
ST **xylose** metab Saccharomyces
IT Biological transport
(of **xylose**, by **Saccharomyces cerevisiae**)
IT **Saccharomyces cerevisiae**

(**xylose** metab. by, pathway for)
IT **58-86-6**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of, by **Saccharomyces cerevisiae**, pathway for)
IT **9028-16-4 99775-25-4**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(of **Saccharomyces cerevisiae**)
IT **58-86-6**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of, by **Saccharomyces cerevisiae**, pathway for)
RN 58-86-6 HCAPLUS
CN D-Xylose (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IT **9028-16-4 99775-25-4**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)
(of **Saccharomyces cerevisiae**)
RN 9028-16-4 HCAPLUS
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 99775-25-4 HCAPLUS
CN Reductase, D-xylose (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

=> sel hit rn l70
E1 THROUGH E14 ASSIGNED

=> fil reg
FILE 'REGISTRY' ENTERED AT 07:18:36 ON 18 MAR 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 17 MAR 2003 HIGHEST RN 499763-93-8
DICTIONARY FILE UPDATES: 17 MAR 2003 HIGHEST RN 499763-93-8

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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               (58-86-6/RN)
             1 64-17-5/BI
               (64-17-5/RN)
             1 9028-16-4/BI
               (9028-16-4/RN)
             1 95829-40-6/BI
               (95829-40-6/RN)
             1 99775-25-4/BI
               (99775-25-4/RN)
             1 50-99-7/BI
               (50-99-7/RN)
             1 9030-58-4/BI
               (9030-58-4/RN)
             1 138263-97-5/BI
               (138263-97-5/RN)
             1 53-57-6/BI
               (53-57-6/RN)
             1 167078-89-9/BI
               (167078-89-9/RN)
             1 167974-35-8/BI
               (167974-35-8/RN)
             1 53-59-8/BI
               (53-59-8/RN)
             1 58-68-4/BI
               (58-68-4/RN)
             1 9028-31-3/BI
               (9028-31-3/RN)
L85         14 (58-86-6/BI OR 64-17-5/BI OR 9028-16-4/BI OR 95829-40-6/BI OR
               99775-25-4/BI OR 50-99-7/BI OR 9030-58-4/BI OR 138263-97-5/BI
               OR 53-57-6/BI OR 167078-89-9/BI OR 167974-35-8/BI OR 53-59-8/BI
               OR 58-68-4/BI OR 9028-31-3/BI)

=> d ide can tot

L85  ANSWER 1 OF 14  REGISTRY  COPYRIGHT 2003 ACS
RN   167974-35-8  REGISTRY
CN   DNA (Saccharoymces cerevisiae strain 1400 clone pLNH33 xylulokinase gene
     plus flanks) (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Deoxyribonucleic acid (Saccharoymces cerevisiae strain 1400 clone pLNH33
     xylulokinase gene plus 5'- and 3'-flanking region fragment)
FS   NUCLEIC ACID SEQUENCE
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS, USPATFULL

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***
               1 REFERENCES IN FILE CA (1962 TO DATE)
               1 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE   1:  123:196764
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L85 ANSWER 2 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **167078-89-9** REGISTRY
CN Xylulokinase (Saccharomyces cerevisiae strain 1400 clone pLNH33 reduced) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

RELATED SEQUENCES AVAILABLE WITH SEQLINK

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***
1 REFERENCES IN FILE CA (1962 TO DATE)
1 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE 1: 123:196764

L85 ANSWER 3 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **138263-97-5** REGISTRY
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (Yamadazyma stipitis clone pUA103 gene XYL1 precursor reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN NADH/NADPH-dependent xylose reductase (Pichia stipitis reduced)
CN Xylose reductase (Pichia stipitis reduced)
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

RELATED SEQUENCES AVAILABLE WITH SEQLINK

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
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5 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE 1: 118:226769

REFERENCE 2: 118:123016

REFERENCE 3: 118:96990

REFERENCE 4: 116:52957

REFERENCE 5: 116:35663

L85 ANSWER 4 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **99775-25-4** REGISTRY
CN Reductase, D-xylose (9CI) (CA INDEX NAME)
OTHER NAMES:
CN D-Xylose reductase
CN NADH-dependent xylose reductase
CN Xylose reductase
MF Unspecified
CI MAN
SR CA
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
47 REFERENCES IN FILE CA (1962 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
47 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE 1: 138:166431

REFERENCE 2: 138:54597

REFERENCE 3: 138:54591

REFERENCE 4: 137:139426

REFERENCE 5: 137:30383

REFERENCE 6: 136:147534

REFERENCE 7: 136:68797

REFERENCE 8: 135:370692

REFERENCE 9: 135:369160

REFERENCE 10: 135:356831

L85 ANSWER 5 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **95829-40-6** REGISTRY
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN D-Xylose reductase
CN NAD(P)H-dependent aldose reductase
CN NAD(P)H-dependent xylose reductase
CN NADPH-D-xylose reductase
CN Xylose reductase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
65 REFERENCES IN FILE CA (1962 TO DATE)
65 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE 1: 138:166431

REFERENCE 2: 137:62252

REFERENCE 3: 137:62211

REFERENCE 4: 137:46120

REFERENCE 5: 137:46093

REFERENCE 6: 135:238477

REFERENCE 7: 135:223348

REFERENCE 8: 134:204861

REFERENCE 9: 133:337140

REFERENCE 10: 133:236908

L85 ANSWER 6 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **9030-58-4** REGISTRY
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN D-Xylulokinase
CN D-Xylulose kinase
CN E.C. 2.7.1.17
CN Xylulokinase
CN Xylulose kinase
DR 57127-28-3
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CIN, EMBASE, PIRA, TOXCENTER, USPATFULL

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115 REFERENCES IN FILE CA (1962 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
115 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE 1: 137:349104

REFERENCE 2: 137:348982

REFERENCE 3: 137:306627

REFERENCE 4: 137:105565

REFERENCE 5: 137:90042

REFERENCE 6: 137:77974

REFERENCE 7: 136:354260

REFERENCE 8: 136:274002

REFERENCE 9: 136:166120

REFERENCE 10: 136:65115

L85 ANSWER 7 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **9028-31-3** REGISTRY
CN Reductase, aldose (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Aldose reductase
CN D-Ribose reductase
CN E.C. 1.1.1.21
CN L-Arabinose reductase
CN NADPH-aldopentose reductase
CN NADPH-aldose reductase
CN NADPH-dependent aldose reductase
CN NADPH-L-arabinose reductase
CN Xylose reductase
MF Unspecified
CI MAN
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CASREACT, CEN, CIN, EMBASE, IFICDB, IFIPAT, IFIUDB, NAPRALERT, PIRA, PROMT, TOXCENTER, USPAT2, USPATFULL

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17 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
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REFERENCE 1: 138:167395

REFERENCE 2: 138:164674

REFERENCE 3: 138:153440

REFERENCE 4: 138:151420

REFERENCE 5: 138:150610

REFERENCE 6: 138:149383

REFERENCE 7: 138:147644

REFERENCE 8: 138:142301

REFERENCE 9: 138:137176

REFERENCE 10: 138:118667

L85 ANSWER 8 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **9028-16-4** REGISTRY
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2,3-cis-Polyol dehydrogenase
CN D-Xylulose reductase
CN Dehydrogenase, 2,3-cis-polyol
CN E.C. 1.1.1.9
CN Erythritol dehydrogenase
CN NAD-dependent meso-erythritol dehydrogenase
CN NAD-dependent xylitol dehydrogenase
CN Polyol dehydrogenase
CN Xylitol dehydrogenase
DR 9032-74-0
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CASREACT, CIN, EMBASE, PIRA, TOXCENTER, USPATFULL

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186 REFERENCES IN FILE CA (1962 TO DATE)
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186 REFERENCES IN FILE CAPLUS (1962 TO DATE)

REFERENCE 1: 138:166431

REFERENCE 2: 138:133152

REFERENCE 3: 137:335006

REFERENCE 4: 137:136757

REFERENCE 5: 137:89412

REFERENCE 6: 137:62252

REFERENCE 7: 137:46120

REFERENCE 8: 137:46116

REFERENCE 9: 137:46093

REFERENCE 10: 136:156403

L85 ANSWER 9 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **64-17-5** REGISTRY
CN Ethanol (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Ethyl alcohol (6CI, 7CI, 8CI)
OTHER NAMES:
CN 100C.NPA
CN AHD 2000
CN Alcare Hand Degermer
CN Alcohol
CN Alcohol anhydrous
CN Algrain
CN Anhydrol
CN Anhydrol PM 4085
CN Desinfektol EL
CN Duplicating Fluid 100C.NPA
CN Esumiru WK 88
CN Ethicap
CN Ethyl hydrate
CN Ethyl hydroxide
CN Hinetoless
CN IMS 99
CN Jaysol
CN Jaysol S
CN Lux
CN Methylcarbinol
CN Molasses alcohol
CN Potato alcohol
CN SDA 3A
CN SDA 40-2
CN SY Fresh M
CN Synasol
CN Tecsol
CN Tecsol C
FS 3D CONCORD
DR 8000-16-6, 8024-45-1, 121182-78-3
MF C2 H6 O
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, AQUIRE, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CANCERLIT, CAOLD, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMINFORMRX, CHEMLIST, CHEMSAFE, CIN, CSCHEM, CSNB, DDFU, DETHERM*, DIOGENES, DIPPR*, DRUGU, EMBASE, ENCOMPLIT, ENCOMPLIT2, ENCOMPPAT, ENCOMPPAT2, GMELIN*, HODOC*, HSDB*, IFICDB, IFIPAT, IFIUDB, IPA, MEDLINE, MRCK*, MSDS-OHS, NAPRALERT, NIOSHTIC, PDLCOM*, PHARMASEARCH, PIRA, PROMT, RTECS*, SPECINFO, TOXCENTER, TULSA, ULIDAT, USAN, USPAT2, USPATFULL, VETU, VTB
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Other Sources: DSL**, EINECS**, TSCA**
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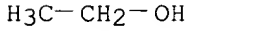

PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

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1120 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

144851 REFERENCES IN FILE CAPLUS (1962 TO DATE)
11 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

REFERENCE 1: 138:179879

REFERENCE 2: 138:179524

REFERENCE 3: 138:179486

REFERENCE 4: 138:179004

REFERENCE 5: 138:178592

REFERENCE 6: 138:178582

REFERENCE 7: 138:178078

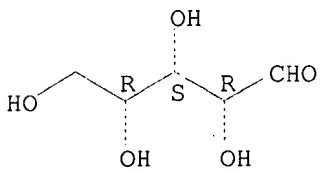
REFERENCE 8: 138:177577

REFERENCE 9: 138:177430

REFERENCE 10: 138:177389

L85 ANSWER 10 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **58-86-6** REGISTRY
CN D-Xylose (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Xylose, D- (8CI)
OTHER NAMES:
CN (+)-Xylose
CN D-(+)-Xylose
CN Wood sugar
CN Xylose
FS STEREOSEARCH
DR 133-56-2, 141492-19-5
MF C5 H10 O5
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CAOLD, CAPLUS, CASREACT, CBNB, CHEMCATS, CHEMINFORMRX, CHEMLIST, CIN, CSCHEM, DDFU, DETHERM*, DIOGENES, DRUGU, EMBASE, GMELIN*, HODOC*, HSDB*, IFICDB, IFIPAT, IFIUDB, IPA, MEDLINE, MRCK*, MSDS-OHS, NAPRALERT, NIOSHTIC, PIRA, PROMT, RTECS*, SPECINFO, SYNTHLINE, TOXCENTER, TULSA, USAN, USPAT2, USPATFULL, VETU, VTB
(*File contains numerically searchable property data)
Other Sources: DSL**, EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

Absolute stereochemistry.



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

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11557 REFERENCES IN FILE CAPLUS (1962 TO DATE)
5 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

REFERENCE 1: 138:172086

REFERENCE 2: 138:172080

REFERENCE 3: 138:172057

REFERENCE 4: 138:169404

REFERENCE 5: 138:169153

REFERENCE 6: 138:168879

REFERENCE 7: 138:166694

REFERENCE 8: 138:166614

REFERENCE 9: 138:166547

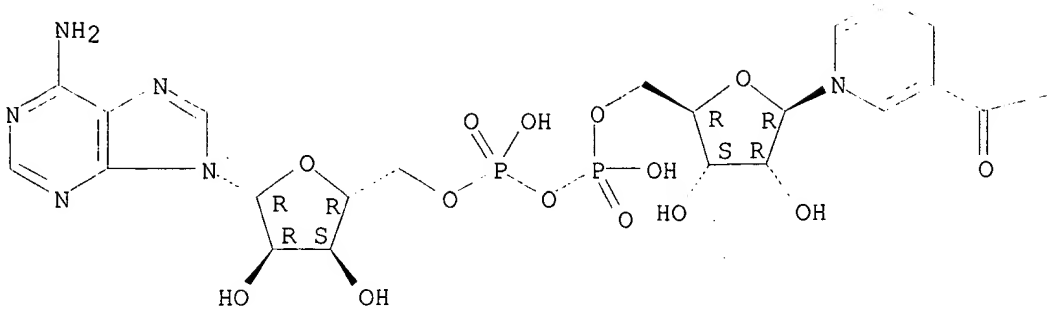
REFERENCE 10: 138:166431

L85 ANSWER 11 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **58-68-4** REGISTRY
CN Adenosine 5'-(trihydrogen diphosphate), P'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosyl-3-pyridinecarboxamide (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Adenosine 5'-(trihydrogen pyrophosphate), 5'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosylnicotinamide (8CI)
CN Adenosine pyrophosphate, 5'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosylnicotinamide (7CI)
OTHER NAMES:
CN .beta.-DPNH
CN .beta.-NADH
CN 1,4-Dihydronicotinamide adenine dinucleotide
CN Codehydrase I, reduced
CN Codehydrogenase I, reduced
CN Coenzyme I, reduced
CN Cozymase I, reduced
CN Dihydrocodehydrogenase I
CN Dihydrocozymase
CN Dihydronicotinamide adenine dinucleotide
CN Dihydronicotinamide mononucleotide
CN DPNH
CN NADH
CN NADH2
CN Nicotinamide-adenine dinucleotide, reduced
CN Reduced codehydrogenase I
CN Reduced diphosphopyridine nucleotide
CN Reduced nicotinamide adenine diphosphate
CN Reduced nicotinamide-adenine dinucleotide
FS STEREOSEARCH
DR 443892-10-2
MF C21 H29 N7 O14 P2
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CAOLD, CAPLUS, CASREACT, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM, DDFU, DRUGU, EMBASE, GMELIN*, IFICDB, IFIPAT, IFIUDB, MRCK*, NIOSHTIC, PROMT, TOXCENTER, USPAT2, USPATFULL
(*File contains numerically searchable property data)

Other Sources: DSL**, EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

—NH_2

PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

12080 REFERENCES IN FILE CA (1962 TO DATE)
217 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
12094 REFERENCES IN FILE CAPLUS (1962 TO DATE)
1 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

REFERENCE 1: 138:175872

REFERENCE 2: 138:173199

REFERENCE 3: 138:168855

REFERENCE 4: 138:168854

REFERENCE 5: 138:166430

REFERENCE 6: 138:166418

REFERENCE 7: 138:166262

REFERENCE 8: 138:166234

REFERENCE 9: 138:166114

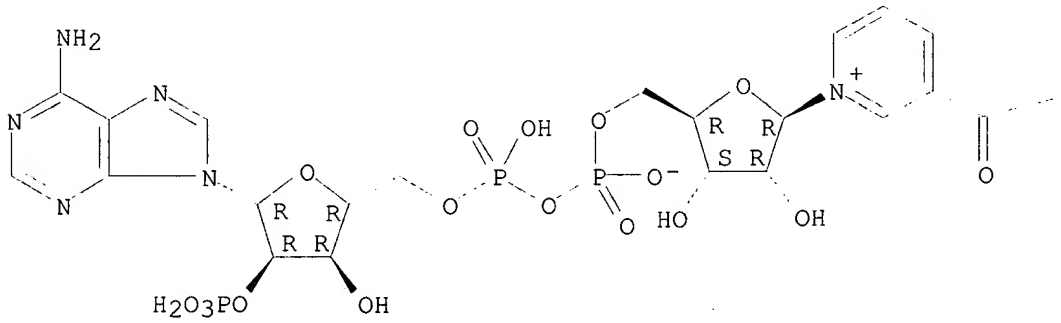
REFERENCE 10: 138:165732

L85 ANSWER 12 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **53-59-8** REGISTRY
CN Adenosine 5'-(trihydrogen diphosphate), 2'-(dihydrogen phosphate), P'.fwdarw.5'-ester with 3-(aminocarbonyl)-1-.beta.-D-ribofuranosylpyridinium, inner salt (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:

CN Adenosine 5'-(trihydrogen diphosphate), 2'-(dihydrogen phosphate), P'.fwdarw.5'-ester with 3-(aminocarbonyl)-1-.beta.-D-ribofuranosylpyridinium hydroxide, inner salt
CN Pyridinium, 3-carbamoyl-1-.beta.-D-ribofuranosyl-, hydroxide, 5'.fwdarw.5'-ester with adenosine 2'-(dihydrogen phosphate) 5'-(trihydrogen pyrophosphate), inner salt (8CI)
OTHER NAMES:
CN .beta.-NADP
CN .beta.-Nicotinamide adenine dinucleotide phosphate
CN .beta.-TPN
CN Adenine-nicotinamide dinucleotide phosphate
CN Codehydrase II
CN Codehydrogenase II
CN Coenzyme II
CN Cozymase II
CN NAD phosphate
CN NADP
CN NADP+
CN Nicotinamide-adenine dinucleotide phosphate
CN TPN
CN TPN (nucleotide)
CN Triphosphopyridine nucleotide
FS STEREOSEARCH
DR 10213-33-9, 162195-92-8, 25158-33-2, 27678-67-7
MF C21 H28 N7 O17 P3
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CANCERLIT, CAOLD, CAPLUS, CASREACT, CHEMCATS, CHEMINFORMRX, CHEMLIST, CIN, CSCHEM, DDFU, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, MEDLINE, MRCK*, NAPRALERT, NIOSHTIC, PIRA, PROMT, RTECS*, TOXCENTER, USPAT2, USPATFULL
(*File contains numerically searchable property data)
Other Sources: DSL**, EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

NH2

5443 REFERENCES IN FILE CA (1962 TO DATE)
197 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

5449 REFERENCES IN FILE CAPLUS (1962 TO DATE)
89 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

REFERENCE 1: 138:175872

REFERENCE 2: 138:166253

REFERENCE 3: 138:165671

REFERENCE 4: 138:165648

REFERENCE 5: 138:165597

REFERENCE 6: 138:163414

REFERENCE 7: 138:152296

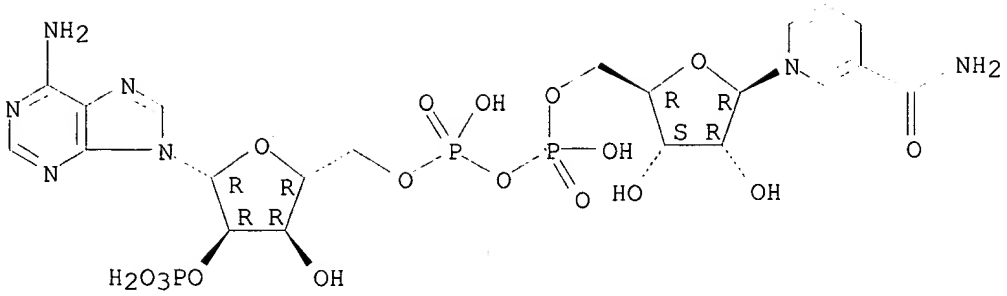
REFERENCE 8: 138:149764

REFERENCE 9: 138:149456

REFERENCE 10: 138:148869

L85 ANSWER 13 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **53-57-6** REGISTRY
CN Adenosine 5'-(trihydrogen diphosphate), 2'-(dihydrogen phosphate), P'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosyl-3-pyridinecarboxamide (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Adenosine, 2'-(dihydrogen phosphate) 5'-(trihydrogen pyrophosphate), 5'.fwdarw.5'-ester with 1,4-dihydro-1-.beta.-D-ribofuranosylnicotinamide (8CI)
OTHER NAMES:
CN .beta.-NADPH
CN .beta.-Nicotinamide-adenine-dinucleotide-phosphoric acid
CN .beta.-TPNH
CN Codehydrase II, reduced
CN Codehydrogenase II, reduced
CN Coenzyme II, reduced
CN Cozymase II, reduced
CN Dihydrocodehydrogenase II
CN NADPH
CN NADPH2
CN Nicotinamide-adenine dinucleotide phosphate, reduced
CN Reduced codehydrogenase II
CN Reduced nicotinamide adenine dinucleotide phosphate
CN Reduced triphosphopyridine nucleotide
CN TPNH
CN Triphosphopyridine nucleotide, reduced
FS STEREOSEARCH
DR 22046-90-8, 3545-01-5
MF C21 H30 N7 O17 P3
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CAOLD, CAPLUS, CASREACT, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM, DDFU, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, MRCK*, NIOSHTIC, PROMT, TOXCENTER, USPAT2, USPATFULL
(*File contains numerically searchable property data)
Other Sources: EINECS**, NDSL**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

Absolute stereochemistry.



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

9623 REFERENCES IN FILE CA (1962 TO DATE)
185 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
9632 REFERENCES IN FILE CAPLUS (1962 TO DATE)
57 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

REFERENCE 1: 138:175872

REFERENCE 2: 138:166262

REFERENCE 3: 138:166253

REFERENCE 4: 138:165997

REFERENCE 5: 138:165782

REFERENCE 6: 138:165732

REFERENCE 7: 138:165659

REFERENCE 8: 138:165648

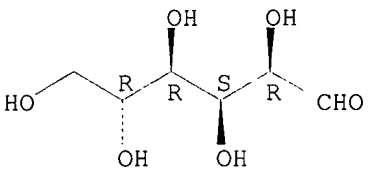
REFERENCE 9: 138:165611

REFERENCE 10: 138:165599

L85 ANSWER 14 OF 14 REGISTRY COPYRIGHT 2003 ACS
RN **50-99-7** REGISTRY
CN D-Glucose (8CI, 9CI) (CA INDEX NAME)
OTHER NAMES:
CN (+)-Glucose
CN Anhydrous dextrose
CN Cartose
CN Cerelose
CN Cerelose 2001
CN Corn sugar
CN D(+)-Glucose
CN Dextropur
CN Dextrose
CN Dextrosol
CN Glucolin
CN Glucose
CN Glucosteril
CN Goldsugar
CN Grape sugar
CN Maxim Energy Gel
CN Roferose ST
CN Staleydex 111

CN Staleydex 333
CN Sugar, grape
CN Tabfine 097(HS)
CN Vadex
FS STEREOSEARCH
DR 8012-24-6, 8030-23-7, 162222-91-5, 165659-51-8, 50933-92-1, 80206-31-1
MF C6 H12 O6
CI COM
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, AQUIRE, BEILSTEIN*, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CANCERLIT, CAOLD, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMINFORMRX, CHEMLIST, CHEMSAFE, CIN, CSCHEM, CSNB, DDFU, DETHERM*, DIOGENES, DIPPR*, DRUGU, EMBASE, GMELIN*, HSDB*, IFICDB, IFIPAT, IFIUDB, IPA, MEDLINE, MRCK*, MSDS-OHS, NAPRALERT, NIOSHTIC, PDLCOM*, PHARMASEARCH, PIRA, PROMT, RTECS*, SPECINFO, TOXCENTER, TULSA, ULIDAT, USAN, USPAT2, USPATFULL, VETU, VTB
(*File contains numerically searchable property data)
Other Sources: DSL**, EINECS**, TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

Absolute stereochemistry.



PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

141620 REFERENCES IN FILE CA (1962 TO DATE)
2054 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
141698 REFERENCES IN FILE CAPLUS (1962 TO DATE)
14 REFERENCES IN FILE CAOLD (PRIOR TO 1967)

REFERENCE 1: 138:179924

REFERENCE 2: 138:179836

REFERENCE 3: 138:178169

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REFERENCE 6: 138:175908

REFERENCE 7: 138:175831

REFERENCE 8: 138:175670

REFERENCE 9: 138:175608

REFERENCE 10: 138:175560

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FILE COVERS 1907 - 18 Mar 2003 VOL 138 ISS 12
FILE LAST UPDATED: 17 Mar 2003 (20030317/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d bib abs hitrn retable tot 171

L71 ANSWER 1 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2003:206363 HCAPLUS
TI Effect of enhanced **xylose reductase** activity on **xylose** consumption and product distribution in **xylose** -fermenting recombinant **Saccharomyces cerevisiae**
AU Jeppsson, Marie; Traff, Karin; Johansson, Bjorn; Hahn-Hagerdal, Barbel; Gorwa-Grauslund, Marie F.
CS Department of Applied Microbiology, Lund University, P.O. Box 124, Lund, 221 00, Swed.
SO FEMS Yeast Research (2003), 3(2), 167-175
CODEN: FYREAG; ISSN: 1567-1356
PB Elsevier Science B.V.
DT Journal
LA English
AB Recombinant **Saccharomyces cerevisiae** TMB3001, harboring the Pichia stipitis genes XYL1 and XYL2 (**xylose reductase** and **xylitol dehydrogenase**, resp.) and the endogenous XKS1(**xylulokinase**), can convert **xylose** to **ethanol**. About 30% of the consumed **xylose**, however, is excreted as xylitol. Enhanced **ethanol** yield has previously been achieved by disrupting the ZWF1 gene, encoding **glucose**-6-phosphate dehydrogenase, but at the expense of the **xylose** consumption. This is probably the result of reduced NADPH-mediated **xylose** redn. In the present study, we increased the **xylose reductase** (XR) activity 4-19 times in both TMB3001 and the ZWF1-disrupted strain TMB3255. The **xylose** consumption rate increased by 70% in TMB3001 under oxygen-limited conditions. In the ZWF1-disrupted background, the increase in XR activity fully restored the **xylose** consumption rate. Maximal specific growth rates on **glucose** were lower in the ZWF1-disrupted strains, and the increased XR activity also neg. affected the growth rate in these strains. Addn. of methionine resulted in 70% and 50% enhanced maximal specific growth rates for TMB3255 (zwf1.DELTA.) and TMB3261 (PGK1-XYL1, zwf1.DELTA.), resp. Enhanced XR activity did not have any neg. effect on the maximal specific growth rate in the control strain. Enhanced glycerol yields were obsd. in the high-XR-activity strains. These are suggested to result from the obsd. reductase activity of the purified XR for dihydroxyacetone phosphate.

L71 ANSWER 2 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2003:48283 HCAPLUS
TI Optimal growth and **ethanol** production from **xylose** by

recombinant **Saccharomyces cerevisiae** require moderate D-**xylulokinase** activity

AU Jin, Yong-Su; Ni, Haiying; Laplaza, Jose M.; Jeffries, Thomas W.

CS Department of Food Science, University of Wisconsin, Madison, WI, 53706, USA

SO Applied and Environmental Microbiology (2003), 69(1), 495-503 CODEN: AEMIDF; ISSN: 0099-2240

PB American Society for Microbiology

DT Journal

LA English

AB D-**Xylulokinase** (XK) is essential for the metab. of D-**xylose** in yeasts. However, overexpression of genes for XK, such as the Pichia stipitis XYL3 gene and the **Saccharomyces cerevisiae** XKS gene, can inhibit growth of **S. cerevisiae** on **xylose**. We varied the copy no. and promoter strength of XYL3 or XKS1 to see how XK activity can affect **xylose** metab. in **S. cerevisiae**. The **S. cerevisiae** genetic background included single integrated copies of P. stipitis XYL1 and XYL2 driven by the **S. cerevisiae** TDH1 promoter. Multicopy and single-copy constructs with either XYL3 or XKS1, likewise under control of the TDH1 promoter, or with the native P. stipitis promoter were introduced into the recombinant **S. cerevisiae**. In vitro enzymic activity of XK increased with copy no. and promoter strength. Overexpression of XYL3 and XKS1 inhibited growth on **xylose** but did not affect growth on **glucose** even though XK activities were three times higher in **glucose**-grown cells. Growth inhibition increased and **ethanol** yields from **xylose** decreased with increasing XK activity. Uncontrolled XK expression in recombinant **S. cerevisiae** is inhibitory in a manner analogous to the substrate-accelerated cell death obsd. with an **S. cerevisiae** tps1 mutant during **glucose** metab. To bypass this effect, we transformed cells with a tunable expression vector contg. XYL3 under the control of its native promoter into the FPL-YS1020 strain and screened the transformants for growth on, and **ethanol** prodn. from, **xylose**. The selected transformant had approx. four copies of XYL3 per haploid genome and had moderate XK activity. It converted **xylose** into **ethanol** efficiently.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Bieche, I	1998	78	661	Int J Cancer	HCAPLUS
Boeke, J	1985	40	491	Cell	HCAPLUS
Chiang, C	1981	42	284	Appl Environ Microbi	
Cho, K	1999	25	23	Enzyme Microb Techno	HCAPLUS
Christianson, T	1992	110	119	Gene	HCAPLUS
De Preter, K	2002	15	159	Mod Pathol	
Hinman, N	1989	20/21	391	Appl Biochem Biotech	
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Hohmann, S	1996	20	981	Mol Microbiol	HCAPLUS
Horiuchi, H	1990	54	1771	Agric Biol Chem	HCAPLUS
Ingham, D	2001	31	132	BioTechniques	HCAPLUS
Jeffries, T	1983	27	1	Adv Biochem Eng Biot	HCAPLUS
Jin, Y				Appl Biochem Biotech	
Jin, Y	2002	68	1232	Appl Environ Microbi	HCAPLUS
Jin, Y	2000	10	564	J Microbiol Biotechn	HCAPLUS
Johansson, B	2001	67	4249	Appl Environ Microbi	HCAPLUS
Kingsman, A	1988	53	333	Cell	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Kurtzman, C	1994	10	1727	Yeast	HCAPLUS
Lai, K	2000	271	392	Biochem Biophys Res	HCAPLUS
Parekh, R	1996	12	16	Biotechnol Prog	HCAPLUS

Richard, P	2000	190	39	FEMS Microbiol Lett	HCAPLUS
Rizzi, M	1989	67	20	J Ferment Bioeng	HCAPLUS
Rodriguez-Pena, J	1998	162	155	FEMS Microbiol Lett	HCAPLUS
Rose, M	1990			Methods in yeast gen	
Senac, T	1990	56	120	Appl Environ Microbi	HCAPLUS
Shamanna, D	1979	139	64	J Bacteriol	HCAPLUS
Sikorski, R	1989	122	19	Genetics	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Microbiol Biote	HCAPLUS
Tantirungkij, M	1993	75	83	J Ferment Bioeng	HCAPLUS
Teusink, B	1998	23	162	Trends Biochem Sci	HCAPLUS
Thevelein, J	1995	20	3	Trends Biochem Sci	HCAPLUS
Toivari, M	2001	3	236	Metab Eng	HCAPLUS
Verduyn, C	1985	226	669	Biochem J	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Wang, P	1980	26	1165	Can J Microbiol	HCAPLUS

L71 ANSWER 3 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:858650 HCAPLUS
DN 138:54597
TI Biological production of xylitol by Candida tropicalis and recombinant **Saccharomyces cerevisiae** containing **xylose reductase** gene
AU Moon, Kwan-Hoon; Lee, Woo-Jong; Kim, Jay-Han; Choi, Jin-Ho; Ryu, Yeon-Woo; Seo, Jin-Ho
CS Department of Food Science and Technology, School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744, S. Korea
SO ACS Symposium Series (2002), 830(Biological Systems Engineering), 53-68
CODEN: ACSMC8; ISSN: 0097-6156
PB American Chemical Society
DT Journal
LA English
OS CASREACT 138:54597
AB Xylitol, a natural sweetener, was produced from **xylose** using Candida tropicalis ATCC 13803 and recombinant **Saccharomyces cerevisiae** contg. the **xylose reductase** gene from Pichia stipitis in various culture modes. A two-substrate fermn. was designed in order to increase xylitol yield and volumetric productivity for C. tropicalis: **glucose** was used for cell growth and **xylose** for xylitol prodn. Computer simulation was undertaken to optimize the two-substrate fermn. using kinetic equations describing rates of cell growth and **xylose** bioconversion as a function of **ethanol** concn. The optimized two-substrate fermn. resulted in xylitol yield of 0.81 g-xylitol/g-**xylose** and volumetric productivity of 5.06 g-xylitol/L.cntdot.hr, which are in good agreement with the computer simulation results. To improve xylitol productivity and final xylitol concn. without sacrificing xylitol yield, cell-recycle fermns. were attempted. A series of cell-recycle expts. showed that the feeding of **xylose**, **glucose** and yeast ext. in the xylitol prodn. phase was the most effective in enhancing xylitol productivity. A metabolically engineered **Saccharomyces cerevisiae** contg. a **xylose reductase** gene from Pichia Stipitis was employed in an attempted to improve xylitol yield further. The recombinant **S. cerevisiae** strain in the optimized fed-batch culture resulted in xylitol yield of 0.95 g-xylitol/g-**xylose** and xylitol productivity of 1.69 g-xylitol/L.cntdot.hr.
IT **50-99-7**, Dextrose, processes **58-86-6**, D-**Xylose**, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(xylitol prodn. by Candida tropicalis and recombinant **Saccharomyces cerevisiae** contg. **xylose reductase** gene)
IT **99775-25-4**, **Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)

(xylitol prodn. by Candida tropicalis and recombinant **Saccharomyces cerevisiae** contg. **xylose reductase** gene)

IT **64-17-5P, Ethanol**, preparation
RL: BYP (Byproduct); PREP (Preparation)
(xylitol prodn. by Candida tropicalis and recombinant **Saccharomyces cerevisiae** contg. **xylose reductase** gene)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Audet, P	1991	1	1	Thermophilicus Int D	
Bruinenberg, P	1983	129	965	J Gen Microb	HCAPLUS
Choi, J	2000	22	1625	Biotechnol Lett	HCAPLUS
Cillilo, V	1968	95	603	J Gen Bacteriol	
Deis, R	1993		94	Food Technol	
Evans, T	1985	243	492	Arch Biochem Biophys	HCAPLUS
Gong, C	1981	3	130	Biotech Lett	
Hallborn, J	1991	9	1090	Bio/Technol	HCAPLUS
Hyoenen, L	1983	28	373	Adv Food Res	
Kim, J	1999	22	181	J Ind Microbiol Biot	HCAPLUS
Kim, S	1997	83	267	J Ferment Bioeng	HCAPLUS
Kotyk, A	1967	12	121	Fol Microbiol	HCAPLUS
Lee, H	1988	110	81	Enz Microb Tech	
Lee, W	2000	35	1199	Process Biochem	HCAPLUS
Meakinen, K	1979	25	137	Adv Food Res	
Meyrial, V	1991	13	281	Biotech Lett	HCAPLUS
Oh, D	1997	25	197	Kor J Appl Microbiol	HCAPLUS
O'Connor, G	1992	39	293	Biotech Bioeng	HCAPLUS
Pepper, T	1988	10	98	Food Technol	
Vongsuvanlert, V	1989	67	35	J Ferment Bioeng	HCAPLUS
Washuttl, J	1973	38	1262	J Food Sci	
Yahash, Y	1996	81	148	J Ferment Bioeng	
Yahashi, Y	1996	18	1395	Biotech Lett	HCAPLUS
Ylikahri, R	1979	25	159	Adv Food Res	HCAPLUS

L71 ANSWER 4 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:762740 HCAPLUS
DN 138:54591
TI Comparison of xylitol production in recombinant **Saccharomyces cerevisiae** strains harboring XYL1 gene of Pichia stipitis and GRE3 gene of **S. cerevisiae**
AU Kim, Myoung-Dong; Jeun, Young-Sok; Kim, Sung-Gun; Ryu, Yeon-Woo; Seo, Jin-Ho
CS Research Center for New Bio-Materials in Agriculture, Department of Food Science and Technology, Seoul National University, Suwon, 441-744, S. Korea
SO Enzyme and Microbial Technology (2002), 31(6), 862-866
CODEN: EMTED2; ISSN: 0141-0229
PB Elsevier Science Inc.
DT Journal
LA English
AB **Xylose reductase** gene of Pichia stipitis (XYL1) and aldose reductase of **Saccharomyces cerevisiae** (GRE3) were expressed in **S. cerevisiae** to explore the xylitol prodn. patterns in batch and fed-batch cultures. Although **glucose** utilization and **ethanol** formation of the two recombinant strains were not different in batch cultures, the xylitol productivity of the strain contg. the **S. cerevisiae** GRE3 gene was 50% of that of the strain harboring the XYL1 gene of P. stipitis. Such a difference in xylitol productivity was confirmed in fed-batch cultures using **ethanol** as a cosubstrate for regeneration of NAD(P)H.

S. cerevisiae GRE3 gene product showed a strong preference to NADPH, while the degrees of cofactor specificity of P. stipitis gene for both NADPH and NADH were almost identical. Similar amts. of **xylose reductase** were expressed in both recombinant strains, but a strict preference to NADPH in the **S. cerevisiae** with the GRE3 gene limited cofactor availability for **xylose** conversion and concomitantly resulted in lower xylitol productivity compared with the recombinant strain contg. the P. stipitis XYL1 gene whose product exhibited almost the same cofactor specificity to NADPH and NADH.

IT **50-99-7**, Dextrose, processes **58-86-6**, D-**Xylose**, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(xylitol prodn. in recombinant **Saccharomyces cerevisiae** harboring XYL1 gene and GRE3 gene)

IT **53-57-6**, NADPH **58-68-4**, NADH **9028-31-3**, Aldose reductase **99775-25-4**, **Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(xylitol prodn. in recombinant **Saccharomyces cerevisiae** harboring XYL1 gene and GRE3 gene)

IT **64-17-5P**, **Ethanol**, preparation
RL: BYP (Byproduct); PREP (Preparation)
(xylitol prodn. in recombinant **Saccharomyces cerevisiae** harboring XYL1 gene and GRE3 gene)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Alexandre, H	2001	498	98	FEBS Lett	HCAPLUS
Aquilera, J	2001	39	273	Curr Genet	
Dieters, W	1975			CH 560175	HCAPLUS
Garay-Arroyo, A	1999	15	879	Yeast	HCAPLUS
Govinden, R	2001	55	76	Appl Microbiol Biote	HCAPLUS
Hallborn, J	1991	9	1090	Biotechnology	HCAPLUS
Hyvoenen, L	1982	28	373	Adv Food Res	
Jeong, E	2001	18	1081	Yeast	HCAPLUS
Jeppson, H	1999	53	92	Appl Microbiol Biote	
Jin, Y	2000	10	564	J Microbiol Biotechn	HCAPLUS
Kim, M	2001	11	564	J Microbiol Biotechn	HCAPLUS
Kuhn, A	1995	6	1580	Appl Environ Microbi	
Lee, H	1998	14	977	Yeast	HCAPLUS
Lee, T	2000	5	27	Biotechnol Bioproces	HCAPLUS
Lee, W	2000	35	1199	Proc Biochem	HCAPLUS
Meinander, N	1994	42	334	Appl Microbiol Biote	HCAPLUS
Meinander, N	1997	54	391	Biotechnol Bioeng	HCAPLUS
Mumber, D	1995	156	119	Gene	
Oh, D	1998	50	419	Appl Microbiol Biote	HCAPLUS
Pepper, T	1988	10	98	Food Technol	
Postama, E	1989	55	468	Appl Environ Microbi	
Rizzi, M	1988	29	148	Appl Microbiol Biote	HCAPLUS
Sambrook, J	1989			Molecular cloning: a	
Schneider, H	1989	55	2877	Appl Environ Microbi	HCAPLUS
Traff, K	2001	67	5668	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 5 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:633211 HCAPLUS
DN 137:348982
TI The non-oxidative pentose phosphate pathway controls the fermentation rate of xylulose but not of **xylose** in **Saccharomyces cerevisiae** TMB3001
AU Johansson, Bjorn; Hahn-Hagerdal, Barbel
CS Department of Applied Microbiology, Lund University, Lund, 221 00, Swed.

SO FEMS Yeast Research (2002), 2(3), 277-282
CODEN: FYREAG; ISSN: 1567-1356
PB Elsevier Science B.V.
DT Journal
LA English
AB **Saccharomyces cerevisiae** is able to ferment **xylose**, when engineered with the enzymes **xylose reductase** (XYL1) and **xylitol dehydrogenase** (XYL2). However, **xylose** fermn. is one to two orders of magnitude slower than **glucose** fermn. **S. cerevisiae** has been proposed to have an insufficient capacity of the non-oxidative pentose phosphate pathway (PPP) for rapid **xylose** fermn. Strains overproducing the non-oxidative PPP enzymes ribulose 5-phosphate epimerase (EC 5.1.3.1), ribose 5-phosphate ketol isomerase (EC 5.3.1.6), transaldolase (EC 2.2.1.2) and transketolase (EC 2.2.1.1), as well as all four enzymes simultaneously, were compared with respect to **xylose** and xylulose fermn. with their **xylose**-fermenting predecessor **S. cerevisiae** TMB3001, expressing XYL1, XYL2 and only overexpressing XKS1 (**xylulokinase**). The level of overprodn. in **S. cerevisiae** TMB3026, overproducing all four non-oxidative PPP enzymes, ranged between 4 and 23 times the level in TMB3001. Overprodn. of the non-oxidative PPP enzymes did not influence the **xylose** fermn. rate in either batch cultures of 50 g l-1 **xylose** or chemostat cultures of 20 g l-1 **glucose** and 20 g l-1 **xylose**. The low specific growth rate on **xylose** was also unaffected. The results suggest that neither of the non-oxidative PPP enzymes has any significant control of the **xylose** fermn. rate in **S. cerevisiae** TMB3001. However, the specific growth rate on xylulose increased from 0.02-0.03 for TMB3001 to 0.12 for the strain overproducing only transaldolase (TAL1) and to 0.23 for TMB3026, suggesting that overproducing all four enzymes has a synergistic effect. TMB3026 consumed xylulose about two times faster than TMB30001 in batch culture of 50 g l-1 xylulose. The results indicate that growth on xylulose and the xylulose fermn. rate are partly controlled by the non-oxidative PPP, whereas control of the **xylose** fermn. rate is situated upstream of **xylulokinase**, in **xylose** transport, in **xylose reductase**, and/or in the **xylitol dehydrogenase**.
IT **64-17-5P**, **Ethanol**, biological studies
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(non-oxidative pentose phosphate pathway controls the fermn. rate of xylulose but not of **xylose** in recombinant **Saccharomyces cerevisiae** TMB3001)
IT **58-86-6**, D **Xylose**, biological studies **9030-58-4**, **Xylulokinase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(non-oxidative pentose phosphate pathway controls the fermn. rate of xylulose but not of **xylose** in recombinant **Saccharomyces cerevisiae** TMB3001)

L71 ANSWER 6 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:529679 HCAPLUS
DN 137:313392
TI **Ethanol** production from enzymatic hydrolysates of sugarcane bagasse using recombinant **xylose**-utilising **Saccharomyces cerevisiae**
AU Martin, Carlos; Galbe, Mats; Wahlbom, C. Fredrik; Hahn-Hagerdal, Barbel; Jonsson, Leif J.
CS Applied Microbiology, Lund University, Lund, SE-221 00, Swed.
SO Enzyme and Microbial Technology (2002), 31(3), 274-282
CODEN: EMTED2; ISSN: 0141-0229
PB Elsevier Science Ireland Ltd.

DT Journal
LA English
AB Sugarcane bagasse was pre-treated by steam explosion at 205 and 215 .degree.C and hydrolyzed with cellulolytic enzymes. The hydrolyzates were subjected to enzymic detoxification by treatment with the phenoloxidase laccase and to chem. detoxification by overliming. Approx. 80% of the phenolic compds. were specifically removed by the laccase treatment. Overliming partially removed the phenolic compds., but also other fermn. inhibitors such as acetic acid, furfural and 5-hydroxy-methyl-furfural. The hydrolyzates were fermented with the recombinant **xylose** -utilizing **Saccharomyces cerevisiae** lab. strain TMB 3001, a CEN.PK deriv. with over-expressed **xylulokinase** activity and expressing the **xylose reductase** and **xylitol dehydrogenase** of Pichia stipitis, and the **S. cerevisiae** strain ATCC 96581, isolated from a spent sulphite liquor fermn. plant. The fermentative performance of the lab strain in undetoxified hydrolyzate was better than the performance of the industrial strain. An almost two-fold increase of the specific productivity of the strain TMB 3001 in the detoxified hydrolyzates compared to the undetoxified hydrolyzates was obsd. The **ethanol** yield in the fermn. of the hydrolyzate detoxified by overliming was 0.18 g/g dry bagasse, whereas it reached only 0.13 g/g dry bagasse in the undetoxified hydrolyzate. Partial **xylose** utilization with low xylitol formation was obsd.
IT **50-99-7P**, Dextrose, preparation **58-86-6P**, D-**Xylose**, preparation
RL: BCP (Biochemical process); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)
(**ethanol** prodn. from enzymic hydrolyzates of sugarcane bagasse using recombinant **xylose**-utilizing **Saccharomyces cerevisiae**)
IT **64-17-5**, **Ethanol**, formation (nonpreparative)
RL: BSU (Biological study, unclassified); FMU (Formation, unclassified); BIOL (Biological study); FORM (Formation, nonpreparative)
(**ethanol** prodn. from enzymic hydrolyzates of sugarcane bagasse using recombinant **xylose**-utilizing **Saccharomyces cerevisiae**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Ashgari, A	1996	16	42	J Ind Microbiol	
Diaz de Villegas, M	1992	12	351	Acta Biotechnol	HCAPLUS
Doran, J	1994	44	240	Biotechnol Bioeng	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Eliasson, A	2000	53	376	Appl Microbiol Biote	HCAPLUS
Galvez, L	2000		3	Handbook of sugarcan	
Gong, C	1993	39/40	83	Appl Biochem Biotech	
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ingram, L	1999	15	277	Biotechnol Progress	
Jeffries, T	1999	65	117	Adv Biochem Eng Biot	HCAPLUS
Jonsson, L	1998	49	691	Appl Microbiol Biote	HCAPLUS
Kaar, W	1998	14	277	Biomass Bioenerg	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Larsson, S	1999	77-79	91	Appl Biochem Biotech	HCAPLUS
Larsson, S	1999	24	151	Enzyme Microb Techno	HCAPLUS
Linden, T	1992	15	103	Appl Environ Microbi	
Maiorella, B	1983	25	103	Biotechnol Bioeng	HCAPLUS
Martin, C	2001	7	361	Proceedings of the S	
Meinander, N	1999	68	79	Bioresource Technol	HCAPLUS
Meinander, N	1997			PhD Thesis, Lund Uni	
Morjanoff, P	1987	29	733	Biotechnol Bioeng	HCAPLUS
Nguyen, Q	1993		321	Bioconversion of for	HCAPLUS

Olsson, L	1996	18	312	Enzyme Microb Techno	HCAPLUS
Palmqvist, E	1999	62	447	Biotechnol Bioeng	HCAPLUS
Palmqvist, E	1999	63	46	Biotechnol Bioeng	HCAPLUS
Puls, J	1993		13	Bioconversion of for	HCAPLUS
Roberto, I	1991	26	15	Process Biochem	HCAPLUS
Saddler, J	1993		73	Bioconversion of for	HCAPLUS
Singleton, V	1999	299	152	Method Enzymol	HCAPLUS
Taherzadeh, M	1996	46	176	Appl Microbiol Biote	HCAPLUS
Van Dijken, J	1986	32	199	FEMS Microbiol Rev	HCAPLUS
Van Zyl, C	1988	17	357	Appl Biochem Biotech	HCAPLUS
Van Zyl, C	1991	13	82	Enzyme Microb Techno	HCAPLUS
Van Zyl, C	1989	135	2791	J Gen Microbiol	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Walfridsson, M	1996	62	4648	Appl Environ Microbi	HCAPLUS
Watson, N	1984	6	451	Enzyme Microb Techno	HCAPLUS

L71 ANSWER 7 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:516601 HCAPLUS
DN 137:83653
TI Methods and compositions for treating cataracts using substances derived from yeast or saltbush with or without chromium
IN Mirsky, Nitsa
PA Natural Compounds Ltd., Israel
SO U.S., 25 pp., Cont.-in-part of U.S. 395,534.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6416794	B1	20020709	US 2000-617865	20000717
	US 6261606	B1	20010717	US 1999-395534	19990914
PRAI	US 1999-395534	A2	19990914		

AB Compns. and methods having anticataract and antiretinopathy activity comprise compds. extd. from natural resources including yeast and saltbush (Atriplex halimus) or synthetic chromium complexes. The compn. is administered orally, parenterally, topically or s.c. For example, the active fractions - GTF, isolated from yeast, and ACMS, isolated from saltbush - inhibited the activity of eye lens aldose reductase, an enzyme which plays an important role in the etiol. of diabetic cataract, by reducing the rate of NADPH oxidn.
IT **50-99-7**, D-**Glucose**, biological studies **9028-31-3**
, Aldose reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(methods and compns. for treating cataract and retinopathy using substances derived from yeast or saltbush with or without chromium)
IT **64-17-5**, **Ethanol**, biological studies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(methods and compns. for treating cataract and retinopathy using substances derived from yeast or saltbush with or without chromium)
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Anderson, R	1977	2	277	Trends in Biochem Sc	
Evans, G	1973	50	718	Biochem Biophys Res	HCAPLUS
Jarrett, R	1982	22	79	Diabetologia	MEDLINE
Jeejebhoy, K	1977	30	531	Am J Clin Nutr	
Lahaye	1991			US 5075116 A	HCAPLUS
Schmidt-Nielsen, K	1964	143	689	Science	MEDLINE
Sivak, J	1986	26	1873	Vision Res	MEDLINE
Thornber	1984	114/6	1070	Journal of Nutrition	
Yamakoshi	1998			US 5804597 A	HCAPLUS

L71 ANSWER 8 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:404531 HCAPLUS
DN 137:139426
TI Stable expression of **xylose reductase** gene enhances xylitol production in recombinant **Saccharomyces cerevisiae**
AU Chung, Yun-Seung; Kim, Myoung-Dong; Lee, Woo-Jong; Ryu, Yeon-Woo; Kim, Ji-Hyeon; Seo, Jin-Ho
CS Department of Food Science and Technology and Research Center for New Bio-Materials in Agriculture, Seoul National University, Suwon, 441-744, S. Korea
SO Enzyme and Microbial Technology (2002), 30(6), 809-816
CODEN: EMTED2; ISSN: 0141-0229
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Effects of the expression mode of the **xylose reductase** gene (XYL1) on xylitol prodn. in recombinant **Saccharomyces cerevisiae** strains were investigated in batch and fed-batch cultures. The gene coding for **xylose reductase** (XR) was introduced into **S. cerevisiae** in two different ways: by using a .delta.-integration vector for chromosome-integration and a YRp-based episomal plasmid vector. The two expression systems showed the different pattern of xylitol prodn. in a **glucose**-limited fed-batch culture as opposed to the similar profile in a batch culture. The recombinant **S. cerevisiae** strain harboring the XR gene in the chromosome yielded a 1.70-fold enhancement in xylitol productivity in the fed-batch culture compared with the YRp-based **xylose reductase** expression strain. Such an improvement for the integrated recombinant strain was supported by the fact that the mitotic stability of the XR gene along with its high expression level worked in a cooperative manner.
IT **50-99-7**, Dextrose, processes **58-86-6**, D-**Xylose**, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(stable expression of **xylose reductase** gene enhances xylitol prodn. in recombinant **Saccharomyces cerevisiae**)
IT **64-17-5P**, **Ethanol**, preparation
RL: BCP (Biochemical process); BYP (Byproduct); BIOL (Biological study); PREP (Preparation); PROC (Process)
(stable expression of **xylose reductase** gene enhances xylitol prodn. in recombinant **Saccharomyces cerevisiae**)
IT **99775-25-4**, **Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(stable expression of **xylose reductase** gene enhances xylitol prodn. in recombinant **Saccharomyces cerevisiae**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Barbosa, M	1988	3	241	J Ind Microbiol	HCAPLUS
Busturia, A	1986	132	379	J Gen Microbiol	HCAPLUS
Dieters, W	1975			CH 560175	HCAPLUS
Govinden, R	2001	55	76	Appl Microbiol Biote	HCAPLUS
Hallborn, J	1994	42	326	Appl Microbiol Biote	HCAPLUS
Hallborn, J	1991	9	1090	Bio/Technology	HCAPLUS
Hyvonen, L	1982	28	373	Adv Food Res	HCAPLUS
Kim, M	2001	85	41	J Biotechnol	HCAPLUS
Lebeau, T	1997	19	615	Biotechnol Lett	HCAPLUS

Lee, F	1997	48	339	Appl Microbiol Biote	HCAPLUS
Lee, W	2000	35	1199	Process Biochem	HCAPLUS
Lopes, T	1991	105	83	Gene	HCAPLUS
Meinander, N	1997	63	1959	Appl Environ Microbi	HCAPLUS
Meinander, N	1994	42	334	Appl Microbiol Biote	HCAPLUS
Meinander, N	1997	54	391	Biotechnol Bioeng	HCAPLUS
Nigam, P	1995	30	117	Process Biochem	HCAPLUS
Parekh, R	1996	12	16	Biotechnol Prog	HCAPLUS
Pepper, T	1988	10	98	Food Technol	
Romanos, M	1992	8	423	Yeast	HCAPLUS
Seo, J	1985	27	1668	Biotechnol Bioeng	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 9 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:295649 HCAPLUS
DN 137:32134
TI Reduced oxidative pentose phosphate pathway flux in recombinant **xylose**-utilizing **Saccharomyces cerevisiae** strains improves the **ethanol** yield from **xylose**
AU Jeppsson, Marie; Johansson, Bjorn; Hahn-Hagerdal, Barbel; Gorwa-Grauslund, Marie F.
CS Department of Applied Microbiology, Lund University, Lund, 221 00, Swed.
SO Applied and Environmental Microbiology (2002), 68(4), 1604-1609
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
OS CASREACT 137:32134
AB In recombinant, **xylose**-fermenting **Saccharomyces cerevisiae**, about 30% of the consumed **xylose** is converted to xylitol. Xylitol prodn. results from a cofactor imbalance, since **xylose reductase** uses both NADPH and NADH, while **xylitol dehydrogenase** uses only NAD+. In this study we increased the **ethanol** yield and decreased the xylitol yield by lowering the flux through the NADPH-producing pentose phosphate pathway. The pentose phosphate pathway was blocked either by disruption of the GND1 gene, one of the isogenes of 6-phosphogluconate dehydrogenase, or by disruption of the ZWF1 gene, which encodes **glucose** 6-phosphate dehydrogenase. Decreasing the phosphoglucose isomerase activity by 90% also lowered the pentose phosphate pathway flux. These modifications all resulted in lower xylitol yield and higher **ethanol** yield than in the control strains. TMB3255, carrying a disruption of ZWF1, gave the highest **ethanol** yield (0.41 g g-1) and the lowest xylitol yield (0.05 g g-1) reported for a **xylose**-fermenting recombinant **S. cerevisiae** strain, but also an 84% lower **xylose** consumption rate. The low **xylose** fermn. rate is probably due to limited NADPH-mediated **xylose** redn. Metabolic flux modeling of TMB3255 confirmed that the NADPH-producing pentose phosphate pathway was blocked and that **xylose** redn. was mediated only by NADH, leading to a lower rate of **xylose** consumption. These results indicate that xylitol prodn. is strongly connected to the flux through the oxidative part of the pentose phosphate pathway.
IT **50-99-7**, Dextrose, processes **58-86-6**, D-**Xylose**, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(reduced oxidative pentose phosphate pathway flux in recombinant **xylose**-utilizing **Saccharomyces cerevisiae** strains improves **ethanol** yield from **xylose**)
IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(reduced oxidative pentose phosphate pathway flux in recombinant **xylose**-utilizing **Saccharomyces cerevisiae**

strains improves **ethanol** yield from **xylose**)
IT **53-57-6**, NADPH **53-59-8**, NADP
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(reduced oxidative pentose phosphate pathway flux in recombinant **xylose**-utilizing **Saccharomyces cerevisiae** strains improves **ethanol** yield from **xylose**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Amore, R	1989	17	7515	Nucleic Acids Res	HCAPLUS
Andreasen, A	1953	41	23	J Cell Comp Physiol	HCAPLUS
Andreasen, A	1954	44	271	J Cell Comp Physiol	
Ausubel, F	1995			Current protocols in	
Benthin, S	1991	5	39	Biotechnol Tech	HCAPLUS
Bergmeyer, H	1974			Methods in enzymatic	
Boles, E	1994	243	363	Mol Gen Genet	MEDLINE
Bruinenberg, P	1983	18	287	Appl Microbiol Biote	HCAPLUS
Bruinenberg, P	1983	129	953	J Gen Microbiol	HCAPLUS
du Preez, J	1987	25	521	Appl Microbiol Biote	HCAPLUS
du Preez, J	1989	152	143	Arch Microbiol	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Eliasson, A	2000	53	376	Appl Microbiol Biote	HCAPLUS
Eliasson, A	2001	29	288	Enzyme Microb Techno	HCAPLUS
Gietz, R	1995	5	255	Methods Mol Cell Bio	
Gonzalez, B	1997	13	1347	Yeast	HCAPLUS
Guldener, U	1996	24	2519	Nucleic Acids Res	MEDLINE
Hallborn, J	1995			PhD thesis, Lund Uni	
Herbert, D	1971	5B	209	Methods Microbiol	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ho, N	1983	13	245	Biotechnol Bioeng Sy	HCAPLUS
Inoue, H	1990	96	23	Gene	HCAPLUS
Johansson, B	2001	67	4249	Appl Environ Microbi	HCAPLUS
Juhnke, H	1996	252	456	Mol Gen Genet	HCAPLUS
Kostrzynska, M	1998	159	107	FEMS Microbiol Lett	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Maitra, P	1971	246	475	J Biol Chem	HCAPLUS
Moes, C	1996	18	269	Biotechnol Lett	HCAPLUS
Nissen, T	1997	143	203	Microbiology	HCAPLUS
Rizzi, M	1988	29	148	Appl Microbiol Biote	HCAPLUS
Rizzi, M	1989	67	20	J Ferment Bioeng	HCAPLUS
Sarthy, A	1987	53	1996	Appl Environ Microbi	HCAPLUS
Sinha, A	1992	138	1865	J Gen Microbiol	HCAPLUS
Skoog, K	1990	56	3389	Appl Environ Microbi	HCAPLUS
Stryer, L	1988			Biochemistry	
Tantirungkij, M	1993	75	83	J Ferment Bioeng	HCAPLUS
Thomas, D	1991	10	547	EMBO J	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
von Sivers, M	1995	51	43	Bioresour Technol	HCAPLUS
Wahlbom, C	2001	72	289	Biotechnol Bioeng	HCAPLUS
Wahlbom, C				Biotechnol Bioeng, i	
Walfridsson, M	1996	62	4648	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Yanisch-Perron, C	1985	33	103	Gene	HCAPLUS
Zhang, Y	1997	147	227	FEMS Microbiol Lett	HCAPLUS

L71 ANSWER 10 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2002:210007 HCAPLUS
DN 137:90042
TI Molecular cloning of XYL3 (D-**xylulokinase**) from Pichia stipitis and characterization of its physiological function
AU Jin, Yong-Su; Jones, Sharon; Shi, Nian-Qing; Jeffries, Thomas W.
CS Department of Food Science, University of Wisconsin, Madison, WI, 53706,

USA
SO Applied and Environmental Microbiology (2002), 68(3), 1232-1239
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB XYL3, which encodes a D-**xylulokinase** (EC 2.7.1.17), was isolated from Pichia stipitis CBS 6054 genomic DNA by using primers designed against conserved motifs. Disruption of XYL3 eliminated D-**xylulokinase** activity, but D-ribulokinase activity was still present. Southern anal. of P. stipitis genomic DNA with XYL3 as a probe confirmed the disruption and did not reveal addnl. related genes. Disruption of XYL3 stopped **ethanol** prodn. from **xylose**, but the resulting mutant still assimilated **xylose** slowly and formed xylitol and arabinitol. These results indicate that XYL3 is crit. for **ethanol** prodn. from **xylose** but that P. stipitis has another pathway for **xylose** assimilation. Expression of XYL3 using its P. stipitis promoter increased **Saccharomyces cerevisiae** D-xylulose consumption threefold and enabled the transformants to produce **ethanol** from a mixt. of **xylose** and xylulose, whereas the parental strain only accumulated xylitol. In vitro, D-**xylulokinase** activity in recombinant **S. cerevisiae** was sixfold higher with a multicopy than with a single-copy XYL3 plasmid, but **ethanol** prodn. decreased with increased copy no. These results confirmed the function of XYL3 in **S. cerevisiae**.
IT **9030-58-4P**, D-**Xylulokinase**
RL: BCP (Biochemical process); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation); PROC (Process)
(mol. cloning of D-**xylulokinase** gene XYL3 from Pichia stipitis and characterization of its physiol. function)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Altschul, S	1990	215	403	J Mol Biol	HCAPLUS
Amore, I	1991	109	89	Gene	
Bork, P	1992	89	7290	Proc Natl Acad Sci U	HCAPLUS
Chang, S	1988	17	313	Appl Biochem Biotech	HCAPLUS
Cho, J	1998	64	1350	Appl Environ Microbi	HCAPLUS
Christianson, T	1992	110	119	Gene	HCAPLUS
Cooper, C	1944	36	504	Ind Eng Chem	HCAPLUS
Dellweg, H	1984	6	395	Biotechnol Lett	HCAPLUS
Du Preez, J	1989	30	53	Appl Microbial Biote	HCAPLUS
Du Preez, J	1983	5	357	Biotechnol Lett	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Eliasson, A	2000	53	376	Appl Microbial Biote	HCAPLUS
Flanagan, T	1992	14	975	Enzyme Microb Teehno	HCAPLUS
Gong, C	1981	20	93	Adv Biochem Eng	HCAPLUS
Grootjen, D	1990	12	20	Enzyme Microb Techno	HCAPLUS
Hallborn, J	1995	11	839	Yeast	HCAPLUS
Ho, N	1999	65	163	Adv Biochem Eng Biot	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ho, N	1989	11	417	Enzyme Microb Techno	HCAPLUS
Jeffries, T	1983	27	1	Adv Biochem Eng Biot	HCAPLUS
Jeffries, T	1999	65	117	Adv Biochem Eng Biot	HCAPLUS
Jeppsson, H	1995	61	2596	Appl Environ Microbi	HCAPLUS
Jin, Y	2000	10	564	J Microbiol Biotechn	HCAPLUS
Johansson, B	2001	67	4249	Appl Environ Microbi	HCAPLUS
Kotter, P	1990	18	493	Curr Genet	MEDLINE
Lawlis, V	1984	47	15	Appl Environ Microbi	HCAPLUS
Lu, P	1998	64	94	Appl Environ Microbi	HCAPLUS

Lu, P	1998	49	141	Appl Microbiol Biote	HCAPLUS
Passoth, V	1998	14	1311	Yeast	HCAPLUS
Reizer, A	1991	5	1081	Mol Microbiol	HCAPLUS
Richard, P	2000	190	39	FEMS Microbiol Lett	HCAPLUS
Rodrignez-Pena, J	1998	162	155	FEMS Microbiol Lett	
Rose, M	1990			Methods in yeast gen	
Rosenfeld, S	1984	194	410	Mol Gen Genet	HCAPLUS
Rothstein, R	1983	101	201	Methods Enzymol	
Saitou, N	1987	4	406	Mol Biol Evol	MEDLINE
Sambrook, J	1989			Molecular cloning: a	
Shamanna, D	1979	139	64	J Bacteriol	HCAPLUS
Shi, N	2000	84-86	201	Appl Biochem Biotech	HCAPLUS
Shi, N	2000			PhD thesis, Universi	
Shi, N	1999	15	1021	Yeast	HCAPLUS
Sikorski, R	1989	122	19	Genetics	HCAPLUS
Slininger, P	1982	26	371	Biotechnol Bioeng	
Stevis, P	1989	20-21	327	Appl Biochem Biotech	
Stevis, P	1987	53	2975	Appl Environ Microbi	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Microbiol Biote	HCAPLUS
Tantirungkij, M	1993	75	83	J Ferm Bioeng	HCAPLUS
Toivari, M	2001	3	236	Metabol Eng	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Weierstall, T	1999	31	871	Mol Microbiol	HCAPLUS
Yang, V	1997	63-65	97	Appl Biochem Biotech	HCAPLUS
Yu, S	1995	44	314	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 11 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:893256 HCAPLUS
DN 136:166120
TI Deletion of the GRE3 aldose reductase gene and its influence on **xylose** metabolism in recombinant strains of **Saccharomyces cerevisiae** expressing the xylA and XKS1 genes
AU Traff, K. L.; Otero Cordero, R. R.; Van Zyl, W. H.; Hahn-Hagerdal, B.
CS Department of Applied Microbiology, Lund University, Lund, 221 00, Swed.
SO Applied and Environmental Microbiology (2001), 67(12), 5668-5674
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB **S. cerevisiae** ferments hexoses efficiently but is unable to ferment **xylose**. When the bacterial enzyme **xylose** isomerase (I) from Thermus thermophilus was produced in **S. cerevisiae, xylose** utilization and **EtOH** formation were demonstrated. In addn., xylitol and acetate were formed. An unspecific aldose reductase (AR) capable of reducing **xylose** to xylitol has been identified in **S. cerevisiae**. The GRE3 gene, encoding the AR enzyme, was deleted in **S. cerevisiae** CEN.PK2-1C, yielding YUSM1009a. I from T. thermophilus was produced, and endogenous **xylulokinase** from **S. cerevisiae** was overproduced in **S. cerevisiae** CEN.PK2-1C and YUSM1009a. In recombinant strains from which the GRE3 gene was deleted, xylitol formation decreased 2-fold. Deletion of the GRE3 gene combined with expression of the xylA gene from T. thermophilus on a replicative plasmid generated recombinant **xylose**-utilizing **S. cerevisiae** strain TMB3102, which produced **EtOH** from **xylose** with a yield of 0.28 mmol C from **EtOH**/mmol C from **xylose**. None of the recombinant strains grew on **xylose**.
IT **58-86-6, Xylose**, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(deletion of the GRE3 aldose reductase gene and its influence on **xylose** metab. in recombinant strains of **Saccharomyces cerevisiae** expressing the xylA and XKS1 genes)

IT **64-17-5P**, **Ethanol**, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(deletion of the GRE3 aldose reductase gene and its influence on **xylose** metab. in recombinant strains of **Saccharomyces cerevisiae** expressing the xylA and XKS1 genes)
IT **9028-31-3**, Aldose reductase **9030-58-4**, **Xylulokinase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(deletion of the GRE3 aldose reductase gene and its influence on **xylose** metab. in recombinant strains of **Saccharomyces cerevisiae** expressing the xylA and XKS1 genes)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Amore, R	1989	30	351	Appl Microbiol Biote	HCAPLUS
Ausubel, F	1995			Current protocols in	
Bolivar, F	1977	2	95	Gene	HCAPLUS
Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
Callens, M	1986	8	696	Enzyme Microb Techno	HCAPLUS
Chan, E	1986	8	231	Biotechnol Lett	HCAPLUS
de Jong-Gubbels, P	1995	11	407	Yeast	HCAPLUS
Du Preez, J	1987	25	521	Appl Microbiol Biote	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Entian, K	1998	26		Yeast gene analysis	HCAPLUS
Garay-Arroyo, A	1999	15	879	Yeast	HCAPLUS
Gietz, R	1995	11	355	Yeast	HCAPLUS
Hayn, M	1993		33	Bioconversion of for	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ho, N	1983	13	245	Biotechnol Bioeng Sy	HCAPLUS
Johansson, B	2001	67	4249	Appl Environ Microbi	HCAPLUS
Kuhn, A	1995	61	1580	Appl Environ Microbi	HCAPLUS
Meinander, N	1997	63	1959	Appl Environ Microbi	HCAPLUS
Moes, C	1996	18	269	Biotechnol Lett	HCAPLUS
Olsson, L	1994	16	388	Enzyme Microb Techno	HCAPLUS
Richard, P	1999	457	135	FEBS Lett	HCAPLUS
Sambrook, J	1989			Molecular cloning:a	
Sarthy, A	1987	53	1996	Appl Environ Microbi	HCAPLUS
Schrunder, J	1996	33	323	Curr Microbiol	MEDLINE
Shamanna, D	1979	139	64	J Bacteriol	HCAPLUS
Sherman, F	1983			Methods in yeast gen	
Skoog, K	1990	56	3389	Appl Environ Microbi	HCAPLUS
Skoog, K	1989	3	1	Biotechnol Tech	HCAPLUS
Southern, E	1975	98	503	J Mol Biol	HCAPLUS
Teusink, B	1998	23	162	Trends Biochem Sci	HCAPLUS
Thestrup, H	1995	61	2043	Appl Environ Microbi	HCAPLUS
Toivari, M	2001	3	236	Metab Eng	HCAPLUS
van Zyl, W	1999	52	829	Appl Microbiol Biote	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Von Sivers, M	1995	51	43	Bioresour Technol	HCAPLUS
Wahlbom, C	2001	72	289	Biotechnol Bioeng	HCAPLUS
Walfridsson, M	1996	62	4648	Appl Environ Microbi	HCAPLUS
Winston, F	1984	107	179	Genetics	HCAPLUS
Yamanaka, K	1969	131	502	Arch Biochem Biophys	HCAPLUS
Yanisch-Perron, C	1985	33	103	Gene	HCAPLUS

L71 ANSWER 12 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:851342 HCAPLUS
DN 135:369160
TI Transgenic **Saccharomyces cerevisiae** expressing genes for enzymes of **xylose** metabolism and its use in fermentation of lignocellulose raw materials to **ethanol**

IN Hahn-haegerdal, Baerbel; Van Zyl, Willhem Herber; Cordero Otero, Ricardo Roman
PA Forskarpatent I Syd, Swed.
SO PCT Int. Appl., 18 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001088094	A1	20011122	WO 2001-SE1061	20010515
W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1282686	A1	20030212	EP 2001-932462	20010515
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRAI ZA 2000-2363 A 20000515
WO 2001-SE1061 W 20010515

AB The present invention relates to a method for obtaining a recombinant yeast of **Saccharomyces cerevisiae** which ferments lignocellulose raw materials to **ethanol**. Genes encoding **xylose reductase** and **xylitol dehydrogenase** from Yamadazyma stipitis and **xylulokinase** from **Saccharomyces cerevisiae** were introduced into yeast for **ethanol** prodn. Furthermore, two **Saccharomyces cerevisiae xylose** fermenting mutant strains XYLUSM125 and XYLUSM145 were created.

IT **50-99-7, Glucose**, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(in growth medium of **Saccharomyces cerevisiae**; transgenic **Saccharomyces cerevisiae** expressing genes for enzymes of **xylose** metab. and its use in fermn. of lignocellulose raw materials to **ethanol**)

IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. to **ethanol** of; transgenic **Saccharomyces cerevisiae** expressing genes for enzymes of **xylose** metab. and its use in fermn. of lignocellulose raw materials to **ethanol**)

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(transgenic **Saccharomyces cerevisiae** expressing genes for enzymes of **xylose** metab. and its use in fermn. of lignocellulose raw materials to **ethanol**)

IT **9028-16-4D, Xylitol dehydrogenase**, variants **9030-58-4D, Xylulokinase**, variants **99775-25-4D , Xylose reductase**, variants
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(transgenic **Saccharomyces cerevisiae** expressing genes for enzymes of **xylose** metab. and its use in fermn. of lignocellulose raw materials to **ethanol**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File

Purdue Research Foundat	1995			WO 9513362 A1	HCAPLUS
Purdue Research Foundat	1997			WO 9742307 A1	HCAPLUS
Tantirungkij, M				Applied Microbiology	

L71 ANSWER 13 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:671127 HCAPLUS
DN 135:356831
TI **Xylulokinase** overexpression in two strains of **Saccharomyces cerevisiae** also expressing **xylose reductase** and **xylitol dehydrogenase** and its effect on fermentation of **xylose** and lignocellulosic hydrolysate
AU Johansson, Bjorn; Christensson, Camilla; Hobley, Timothy; Hahn-Hagerdal, Barbel
CS Department of Applied Microbiology, Lund University, Lund, 221 00, Swed.
SO Applied and Environmental Microbiology (2001), 67(9), 4249-4255
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB Fermn. of the pentose sugar **xylose** to **ethanol** in lignocellulosic biomass would make bioethanol prodn. economically more competitive. **Saccharomyces cerevisiae**, an efficient **ethanol** producer, can utilize **xylose** only when expressing the heterologous genes XYL1 (**xylose reductase**) and XYL2 (**xylitol dehydrogenase**). **Xylose reductase** and **xylitol dehydrogenase** convert **xylose** to its isomer xylulose. The gene XKS1 encodes the xylulose-phosphorylating enzyme **xylulokinase**. In this study, we detd. the effect of XKS1 overexpression on two different **S. cerevisiae** host strains, H158 and CEN.PK, also expressing XYL1 and XYL2. H158 has been previously used as a host strain for the construction of recombinant **xylose**-utilizing **S. cerevisiae** strains. CEN.PK is a new strain specifically developed to serve as a host strain for the development of metabolic engineering strategies. Fermn. was carried out in defined and complex media contg. a hexose and pentose sugar mixt. or a birch wood lignocellulosic hydrolyzate. XKS1 overexpression increased the **ethanol** yield by a factor of 2 and reduced the xylitol yield by 70 to 100% and the final acetate concns. by 50 to 100%. However, XKS1 overexpression reduced the total **xylose** consumption by half for CEN.PK and to as little as one-fifth for H158. Yeast ext. and peptone partly restored sugar consumption in hydrolyzate medium. CEN.PK consumed more **xylose** but produced more xylitol than H158 and thus gave lower **ethanol** yields on consumed **xylose**. The results demonstrate that strain background and modulation of XKS1 expression are important for generating an efficient **xylose**-fermenting recombinant strain of **S. cerevisiae**.
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(**xylulokinase** overexpression in two strains of **Saccharomyces cerevisiae** also expressing **xylose reductase** and **xylitol dehydrogenase** and its effect on fermn. of **xylose** and lignocellulosic hydrolyzate)
IT **50-99-7**, Dextrose, biological studies
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(**xylulokinase** overexpression in two strains of **Saccharomyces cerevisiae** also expressing **xylose reductase** and **xylitol**

dehydrogenase and its effect on fermn. of **xylose** and lignocellulosic hydrolyzate)

IT **58-86-6**, D-**Xylose**, biological studies **9028-16-4**, **Xylitol dehydrogenase 9030-58-4**, **Xylulokinase 99775-25-4**, **Xylose reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**xylulokinase** overexpression in two strains of **Saccharomyces cerevisiae** also expressing **xylose reductase** and **xylitol dehydrogenase** and its effect on fermn. of **xylose** and lignocellulosic hydrolyzate)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Ausubel, F	1995			Current protocols in	
Bachmair, A	1986	234	179	Science	HCAPLUS
Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
de Jong-Gubbels, P	1995	11	407	Yeast	HCAPLUS
Deng, X	1990	24/25	193	Appl Biochem Biotech	
Dobson, M	1982	10	2625	Nucleic Acids Res	HCAPLUS
D'Amore, T	1989	11	411	Enzyme Microb Techno	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Eliasson, A	2000	53	376	Appl Microbiol Biote	HCAPLUS
Entian, K	1998	26	431	Methods Microbiol	HCAPLUS
Gietz, R	1988	74	527	Gene	HCAPLUS
Gietz, R	1994		121	Molecular genetics o	HCAPLUS
Guthrie, C	1991	194	552	Methods Enzymol	
Hahn-Hagerdal, B				Adv Biochem Eng Biot	
Hallborn, J	1994	42	326	Appl Microbiol Biote	HCAPLUS
Hallborn, J	1991	9	1090	Bio/Technology	HCAPLUS
Ho, N	1993			US 5789210	HCAPLUS
Ho, N	1999	65	163	Adv Biochem Eng Biot	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Jeffries, T	1999	65	117	Adv Biochem Eng Biot	HCAPLUS
Kilian, S	1988	27	545	Appl Microbiol Biote	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
La Grange, D	1996	62	1036	Appl Environ Microbi	HCAPLUS
Larsson, S	1999	24	151	Enzyme Microb Techno	HCAPLUS
Looman, A	1993	21	4268	Nucleic Acids Res	HCAPLUS
Meinander, N	1997	63	1959	Appl Environ Microbi	HCAPLUS
Meinander, N	1999	68	79	Bioresource Technol	HCAPLUS
Meinander, N	1996	142	165	Microbiology	HCAPLUS
Mellor, J	1983	24	1	Gene	HCAPLUS
Palmqvist, E	1999	62	447	Biotechnol Bioeng	HCAPLUS
Payne, G	1987	7	3888	Mol Cell Biol	HCAPLUS
Rodriguez-Pena, J	1998	162	155	FEMS Microbiol Lett	HCAPLUS
Sambrook, J	1989			Molecular cloning:a	
Shamanna, D	1979	139	64	J Bacteriol	HCAPLUS
Sherman, F	1983			Methods in yeast gen	
Taherzadeh, M	1997	36	4659	Ind Eng Chem Res	HCAPLUS
Tantirungkij, M	1993	75	83	J Ferment Bioeng	HCAPLUS
Tettelin, H	1997	387	81	Nature	HCAPLUS
Teusink, B	1998	23	162	Trends Biochem Sci	HCAPLUS
van Dijken, J	2000	26	706	Enzyme Microb Techno	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Von Sivers, M	1995	51	43	Bioresource Technol	HCAPLUS
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1996	62	4648	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Wang, P	1980	26	1165	Can J Microbiol	HCAPLUS

L71 ANSWER 14 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:626680 HCAPLUS
DN 135:343382
TI The **xylose reductase/xylitol dehydrogenase/xylulokinase** ratio affects product formation in recombinant **xylose**-utilizing **Saccharomyces cerevisiae**
AU Eliasson, A.; Hofmeyr, J.-H. S.; Pedler, S.; Hahn-Hagerdal, B.
CS Department of Applied Microbiology, Lund University, Lund, SE-221 00, Swed.
SO Enzyme and Microbial Technology (2001), 29(4-5), 288-297
CODEN: EMTED2; ISSN: 0141-0229
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Data simulations based on a kinetic model implied that under simplified simulation conditions a 1:.gtoreq.10:.gtoreq.4 relation of the **xylose reductase** (XR)/**xylitol dehydrogenase** (XDH)/**xylulokinase** (XK) ratio was optimal in minimizing xylitol formation during **xylose** utilization in yeast. The steady-state level of the intermediary xylitol depended also, to a great extent, on the NADH and NAD+ concns. Anaerobic **xylose** utilization was investigated for three different recombinant, XR-, XDH- and XK-expressing **Saccharomyces cerevisiae** strains, TMB 3002, TMB 3003 and TMB 3004, to verify the model predictions. Overexpression of XK was found to be necessary for **ethanol** formation from **xylose**. Furthermore, the xylitol formation decreased with decreasing XR/XDH ratio, while the **ethanol** formation increased. Of the three strains, TMB 3004, which was the strain with a XR/XDH/XK ratio corresponding to the theor. optimal ratio, fermented **xylose** to **ethanol** most efficiently.
IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(**xylose reductase/xylitol dehydrogenase/xylulokinase** ratio affects product formation in recombinant **xylose**-utilizing **Saccharomyces cerevisiae**)
IT **58-86-6**, D-**Xylose**, biological studies **9028-16-4, Xylitol dehydrogenase 9030-58-4, Xylulokinase 99775-25-4, Xylose reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**xylose reductase/xylitol dehydrogenase/xylulokinase** ratio affects product formation in recombinant **xylose**-utilizing **Saccharomyces cerevisiae**)
IT **53-84-9**, NAD **58-68-4**, NADH
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(**xylose reductase/xylitol dehydrogenase/xylulokinase** ratio affects product formation in recombinant **xylose**-utilizing **Saccharomyces cerevisiae**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Ammerer, G	1983	101	192	Meth Enzymol	HCAPLUS
Andreasen, A	1953	41	23	J Cell Comp Physiol	HCAPLUS

Andreasen, A	1954	43	271	J Cell Comp Physiol	HCAPLUS
Bailey, J	1993	48	29	Adv Biochem Eng	MEDLINE
Bergmeyer, H	1985	2		Methods of enzymatic	
Bertani, G	1952	62	293	J Bact	
Chambers, A	1989	9	5516	Mol Cell Biol	HCAPLUS
Christensen, I	1995	50	2601	Chem Eng Sci	
Cornish-Bowden, A	1995	23	439	Bioorg Chem	HCAPLUS
de Jong-Gubbels, P	1995	11	407	Yeast	HCAPLUS
Deng, X	1990	25	193	Appl Biochem Biotech	
Denis, C	1983	258	1165	J Biol Chem	HCAPLUS
du Preez, J	1989	152	143	Arch Microbiol	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Eliasson, A	2000	53	376	Appl Microbiol Biote	HCAPLUS
Eliasson, A	2000			PhD thesis, Lund Uni	
Flanagan, T	1992	14	975	Enzyme Microb Techno	HCAPLUS
Gietz, R	1988	74	527	Gene	HCAPLUS
Gopal, C	1989	30	160	Appl Microbiol Biote	HCAPLUS
Hallborn, J	1994	42	326	Appl Microbiol Biote	HCAPLUS
Hayn, M	1993		33	Bioconversion of for	HCAPLUS
Hinman, N	1992	35	639	Appl Biochem Biotech	
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Hofmeyr, J	2000	476	47	FEBS Lett	HCAPLUS
Inoue, H	1990	96	23	Gene	HCAPLUS
Janes, M	1990	18	97	Curr Genet	HCAPLUS
Jeppsson, H	1999	53	92	Appl Microbiol Biote	HCAPLUS
Johansson, B				submitted	
Koch, A	1983	19	455	J Mol Evol	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Lynd, L	1991	251	1318	Science	HCAPLUS
Meinander, N	1997	54	391	Biotech Bioeng	HCAPLUS
Mendes, P	1993	9	563	Comp Appl Biosci	HCAPLUS
Palmqvist, E	1999	62	447	Biotechnol Bioeng	HCAPLUS
Rizzi, M	1988	29	148	Appl Microbiol Biote	HCAPLUS
Rizzi, M	1989	67	20	J Ferment Bioeng	HCAPLUS
Rizzi, M	1989	67	25	J Ferment Bioeng	HCAPLUS
Sambrook, J	1989			Molecular cloning: a	
Schaaff, I	1989	5	285	Yeast	HCAPLUS
Schiestl, R	1989	16	339	Curr Genet	HCAPLUS
Sherman, F	1991	194	3	Meth Enzymol	HCAPLUS
Sherman, F	1983			Methods in yeast gen	
Skoog, K	1990	56	3389	Appl Environ Microbi	HCAPLUS
Snoep, J	1995	141	2329	Microbiology	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Microbiol Biote	HCAPLUS
Teusink, B	1998	23	162	TiBS	HCAPLUS
Tuite, M	1982	1	603	EMBO J	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
von Sivers, M	1995	51	43	Biores Technol	HCAPLUS
Wahlbom, F				submitted	
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 15 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:545704 HCAPLUS
DN 135:136473
TI Manufacture of five-carbon sugars and sugar alcohols using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway
IN Miasnikov, Andrei; Ojamo, Heikki; Povelainen, Mira; Gros, Hakan; Toivari, Mervi; Richard, Peter; Ruohonen, Laura; Koivuranta, Kari; Londesborough, John; Aristidou, Aristos; Penttilae, Merja; Plazanet-Menut, Claire; Deutscher, Josef
PA Xyrofin Oy, Finland
SO PCT Int. Appl., 205 pp.

CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001053306	A2	20010726	WO 2001-FI51	20010122
	WO 2001053306	A3	20020418		
	W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 2001031784	A5	20010731	AU 2001-31784	20010122
	BR 2001007918	A	20021105	BR 2001-7918	20010122
	EP 1254244	A2	20021106	EP 2001-903815	20010122
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRAI	US 2000-488581	A	20000121		
	WO 2001-FI51	W	20010122		

AB The invention relates to the methods of manufg. five-carbon sugars and sugar alcs. as well as other compds. derived from pentose-phosphate pathway (PPP) from readily available substrates such a hexoses using metabolically engineered microbial hosts. A series of the genes involved in the PPP are cloned from various microorganisms or disrupted in the host of either Bacillus subtilis or **Saccharomyces cerevisiae** . This strategy is demonstrated to successfully increase the yield of a variety of the five-carbon sugar or sugar alcs. for manufg. purpose.

IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermn. of; manuf. of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway)

IT **50-99-7**, D-**Glucose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(five carbon sugar or sugar alc. fermn. from; manuf. of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway)

IT **58-86-6P**, **Xylose**, biological studies
RL: BMF (Bioindustrial manufacture); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process)
(manuf. of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway)

IT **53-57-6**, NADPH **53-59-8**, NADP **53-84-9**, NAD
58-68-4, NADH
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(manuf. of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway)

IT **9030-58-4**, **Xylulokinase**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(manuf. of five-carbon sugars and sugar alcs. using microorganisms

deficient in or transformed with genes involved in pentose-phosphate pathway)

IT **9028-16-4, Xylitol dehydrogenase**
99775-25-4, Xylose reductase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(manuf. of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway)

IT **104118-53-8, Xylose reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); CAT (Catalyst use); BIOL (Biological study); PROC (Process); USES (Uses)
(redox system using; manuf. of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with genes involved in pentose-phosphate pathway)

L71 ANSWER 16 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:524614 HCAPLUS
DN 135:271957
TI Expression of bifunctional enzymes with **xylose reductase** and **xylitol dehydrogenase** activity in **Saccharomyces cerevisiae** alters product formation during **xylose** fermentation
AU Anderlund, Mikael; Radstrom, Peter; Hahn-Hagerdal, Barbel
CS Department of Applied Microbiology, Lund University, Lund, Swed.
SO Metabolic Engineering (2001), 3(3), 226-235
CODEN: MEENFM; ISSN: 1096-7176
PB Academic Press
DT Journal
LA English
AB To enhance metabolite transfer in the two initial sequential steps of **xylose** metab. in yeast, two structural genes of Pichia stipitis, XYL1 and XYL2 encoding **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH), resp., were fused in frame. Four chimeric genes were constructed, encoding fusion proteins with different orders of the enzymes and different linker lengths. These genes were expressed in **Saccharomyces cerevisiae**. The fusion proteins exhibited both XR and XDH activity when XYL1 was fused downstream of XYL2. The specific activity of the XDH part of the complexes increased when longer peptide linkers were used. Bifunctional enzyme complexes, analyzed by gel filtration, were found to be tetramers, hexamers, and octamers. No degrdn. products were detected by Western blot anal. **S. cerevisiae** strains harboring the bifunctional enzymes grew on minimal-medium **xylose** plates, and oxygen-limited **xylose** fermn. resulted in **xylose** consumption and **ethanol** formation. When a fusion protein, contg. a linker of three amino acids, was coexpressed with native XR and XDH monomers in **S. cerevisiae**, enzyme complexes consisting of chimerical and native subunits were formed. The total activity of these complexes showed XR and XDH activities similar to the activities obtained when the monomers were expressed individually. Strains which coexpressed chimerical subunits together with native XR and XDH monomers consumed less **xylose** and produced less xylitol. However, the xylitol yield was lower in these strains than in strains expressing only native XR and XDH monomers, 0.55 and 0.62, resp., and the **ethanol** yield was higher. The reduced xylitol yield was accompanied by reduced glycerol and acetate formation suggesting enhanced utilization of NADH in the XR reaction. (c) 2001 Academic Press.

IT **58-86-6, Xylose**, biological studies **9028-31-3, Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression of bifunctional enzymes with **xylose reductase** and **xylitol dehydrogenase**

activity in **Saccharomyces cerevisiae** alters product formation during **xylose** fermn.)

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermn.; expression of bifunctional enzymes with **xylose reductase** and **xylitol dehydrogenase** activity in **Saccharomyces cerevisiae** alters product formation during **xylose** fermn.)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
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Ammerer, G	1983	101	192	Methods Enzymol	HCAPLUS
Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
Bruinenberg, P	1984	19	256	Appl Microbiol Biote	HCAPLUS
Bruinenberg, P	1983	18	287	Eur J Appl Microbiol	HCAPLUS
Buelow, L	1987	163	443	Eur J Biochem	HCAPLUS
Carlsson, H	1996	1293	154	Biochim Biophys Acta	HCAPLUS
Carlsson, H	1992	14	439	Biotechnol Lett	HCAPLUS
Chang, S	1990	23	363	Acc Chem Res	HCAPLUS
Crawford, I	1987	262	239	J Biol Chem	HCAPLUS
Curtis, B	1991	88	5809	Proc Natl Acad Sci	HCAPLUS
De Moraes, P	1995	43	1067	Appl Microbiol Biote	
Easterby, J	1981	199	155	Biochem J	HCAPLUS
Elcock, A	1996	35	12652	Biochemistry	HCAPLUS
Hallborn, J	1991	9	1090	Biotechnology	HCAPLUS
Keleti, T	1984	223	299	Biochem J	HCAPLUS
Kholodenko, B	1996	389	123	FEBS Lett	HCAPLUS
Kholodenko, J	1996	313	921	Biochem J	
Koetter, P	1993	38	776	Appl Microbiol Biote	HCAPLUS
Koetter, P	1990	18	493	Curr Genet	HCAPLUS
Kuhn, A	1995	61	1580	Appl Environ Microbi	HCAPLUS
Laemmli, U	1970	227	680	Nature	HCAPLUS
Liden, G	1996	62	3894	Appl Environ Microbi	HCAPLUS
Lindbladh, C	1994	33	11684	Biochemistry	HCAPLUS
Lindbladh, C	1992	204	241	Eur J Biochem	HCAPLUS
Lindbladh, C	1992			Thesis Lund Univ	
Linden, T	1989	3	189	Biotechnol Tech	HCAPLUS
Ljungcrantz, P	1989	28	8786	Biochemistry	HCAPLUS
Meinander, N	1996	142	165	Microbiology	HCAPLUS
Mellor, J	1983	24	1	Gene	HCAPLUS
Murley, L	1995	34	10358	Biochemistry	HCAPLUS
Oura, E	1977	12	19	Process Biochem	HCAPLUS
Ovadi, J	1991	152	1	J Theor Biol	HCAPLUS
Purvis, I	1987	193	417	J Mol Biol	
Rhee, I	1990	3	205	Protein Eng	HCAPLUS
Rizzi, M	1988	29	148	Appl Microbiol Biote	HCAPLUS
Rizzi, M	1989	67	20	J Ferment Bioeng	HCAPLUS
Rock, F	1992	5	583	Protein Eng	HCAPLUS
Rose, M	1990			Methods in Yeast Gen	
Sambrook, J	1989			Molecular Cloning: A	
Schiestl, R	1989	16	339	Curr Genet	HCAPLUS
Sherman, F	1983			Methods in Yeast Gen	
Shibuya, I	1992	56	884	Biosci Biotechnol Bi	HCAPLUS
Smiley, K	1982	4	607	Biotechnol Lett	HCAPLUS
Srere, P	1987	56	89	Annu Rev Biochem	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Biotechnol Bioc	HCAPLUS
Tantirungkij, M	1993	75	83	J Ferment Bioeng	HCAPLUS
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Yanisch-Perron, C	1985	33	103	Gene	HCAPLUS

Zalkin, H |1984 |259 |3985 |J Biol Chem |HCAPLUS

L71 ANSWER 17 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:524607 HCAPLUS
DN 135:370692
TI Conversion of **Xylose** to **Ethanol** by Recombinant **Saccharomyces cerevisiae**: Importance of **Xylulokinase** (XKS1) and Oxygen Availability
AU Toivari, Mervi H.; Aristidou, Aristos; Ruohonen, Laura; Penttila, Merja
CS VTT Biotechnology, FIN-02044, Finland
SO Metabolic Engineering (2001), 3(3), 236-249
CODEN: MEENFM; ISSN: 1096-7176
PB Academic Press
DT Journal
LA English
AB The yeast **Saccharomyces cerevisiae** efficiently ferments hexose sugars to **ethanol**, but it is unable to utilize **xylose**, a pentose sugar abundant in lignocellulosic materials. Recombinant strains contg. genes coding for **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH) from the **xylose**-utilizing yeast Pichia stipitis have been reported; however, such strains ferment **xylose** to **ethanol** poorly. One reason for this may be the low capacity of **xylulokinase**, the third enzyme in the **xylose** pathway. To investigate the potential limitation of the **xylulokinase** step, we have overexpressed the endogenous gene for this enzyme (XKS1) in **S. cerevisiae** that also expresses the P. stipitis genes for XR and XDH. The metab. of this recombinant yeast was further investigated in pure **xylose** bioreactor cultivation at various oxygen levels. The results clearly indicated that overexpression of XKS1 significantly enhances the specific rate of **xylose** utilization. In addn., the XK-overexpressing strain can more efficiently convert **xylose** to **ethanol** under all aeration conditions studied. One of the important illustrations is the significant anaerobic and aerobic **xylose** conversion to **ethanol** by the recombinant Saccharomyces; moreover, this was achieved on pure **xylose** as a carbon. Under microaerobic conditions, 5.4 g L-1 **ethanol** was produced from 47 g L-1 **xylose** during 100 h. In fed-batch cultivations using a mixt. of **xylose** and **glucose** as carbon sources, the specific **ethanol** prodn. rate was highest at the highest aeration rate tested and declined by almost one order of magnitude at lower aeration levels. Intracellular metabolite analyses and in vitro enzyme activities suggest the following: the control of flux in a strain that overexpresses XKS1 has shifted to the nonoxidative steps of the pentose phosphate pathway (i.e., downstream of **xylose** 5-phosphate), and enzymic steps in the lower part of glycolysis and **ethanol** formation pathways (pyruvate kinase, pyruvate decarboxylase, and alc. dehydrogenase) do not have a high flux control in this recombinant strain. Furthermore, the intracellular ATP levels were found to be significantly lower for the XK strain compared with either the control strain under similar conditions or **glucose** -grown Saccharomyces. The ATP : ADP ratios were also lower for the XK strain, esp. under microaerobic conditions (0.9 vs 6.4). (c) 2001 Academic Press.
IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(importance of **xylulokinase** and oxygen in the conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae**)
IT **50-99-7**, Dextrose, biological studies **58-86-6**, D-**Xylose**, biological studies **9030-58-4**, **Xylulokinase** **99775-25-4**, **Xylose**

reductase
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(importance of **xylulokinase** and oxygen in the conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae**)

IT **56-65-5**, Adenosine triphosphate, biological studies **58-64-0**, Adenosine diphosphate, biological studies **61-19-8**, Adenosine monophosphate, biological studies
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(importance of **xylulokinase** and oxygen in the conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae**)

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Boles, E	1993	160	324	Arch Microbiol	HCAPLUS
Boles, E	1996	20	65	Mol Microbiol	HCAPLUS
Boles, E	1993	9	761	Yeast	HCAPLUS
Cao, N	1996	18	1013	Biotechnol Lett	HCAPLUS
Cutress, T	1992	59	313	Am Soc Dent Child J	MEDLINE
de Koning, W	1992	204	118	Anal Biochem	HCAPLUS
Denis, C	1983	258	1165	J Biol Chem	HCAPLUS
Denis, C	1981	148	355	J Mol Biol	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Flikweert, M	1996	12	247	Yeast	HCAPLUS
Forbord, B	1992	24	509	Int J Biochem	HCAPLUS
Gancedo, J	1973		193	Plant Sci Lett	HCAPLUS
Gietz, D	1992	20	1425	Nucleic Acids Res	HCAPLUS
Gietz, R	1988	74	527	Gene	HCAPLUS
Hill, J	1991	19	5791	Nucleic Acids Res	HCAPLUS
Hill, J	1991	19	6688	published erratum ap	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ho, N	1989	11	417	Enzyme Microb Techno	HCAPLUS
Koetter, P	1993	38	776	Appl Microbiol Biote	HCAPLUS
Koetter, P	1990	18	493	Curr Genet	HCAPLUS
Larsson, C	2000	16	797	Yeast	HCAPLUS
Liesen, T	1996	21	621	Mol Microbiol	HCAPLUS
Mellor, J	1983	24	1	Gene	HCAPLUS
Metzger, M	1994	42	319	Appl Microbiol Biote	HCAPLUS
Muller, S	1995	177	4517	J Bacteriol	MEDLINE
Richard, P	1999	457	135	FEBS Lett	HCAPLUS
Richard, P	2000	190	39	FEMS Microbiol Lett	HCAPLUS
Rodriguez-Pena, J	1998	162	155	FEMS Microbiol Lett	HCAPLUS
Ruohonen, L	1995	39	193	J Biotechnol	HCAPLUS
Sambrook, J	1989			Molecular Cloning: A	
Schmitt, H	1983	192	247	Mol Gen Genet	HCAPLUS
Seeboth, P	1990	172	678	J Bacteriol	HCAPLUS
Senac, T	1990	56	120	Appl Environ Microbi	HCAPLUS
Sherman, F	1983			Methods in Yeast Gen	
Small, W	1998	180	4051	J Bacteriol	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Microbiol Biote	HCAPLUS
Vallari, R	1992	12	1663	Mol Cell Biol	HCAPLUS
van Hoek, P	1998	64	2133	Appl Environ Microbi	HCAPLUS
van Zyl, W	1999	52	829	Appl Microbiol Biote	HCAPLUS
Vincent, M	1989	253A	317	Adv Exp Med Biol	HCAPLUS
Vincent, M	1989	3	1862	FASEB J	HCAPLUS
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Woodcock, D	1989	17	3469	Nucleic Acids Res	HCAPLUS

Yamamoto, T	1993	31	35	Int J Clin Pharmacol	HCAPLUS
Yamamoto, T	1996	45	1354	Metab Clin Exp	HCAPLUS
Yang, V			97	Appl Biochem Biotech	
Yang, V	1997		63	Appl Biochem Biotech	
Yu, S	1995	44	314	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 18 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:59446 HCAPLUS
DN 134:251284
TI Intracellular fluxes in a recombinant **xylose**-utilizing **Saccharomyces cerevisiae** cultivated anaerobically at different dilution rates and feed concentrations
AU Wahlbom, C. Fredrik; Eliasson, Anna; Hahn-Hagerdal, Barbel
CS Department of Applied Microbiology, Lund University, Lund, SE-221 00, Swed.
SO Biotechnology and Bioengineering (2001), 72(3), 289-296
CODEN: BIBIAU; ISSN: 0006-3592
PB John Wiley & Sons, Inc.
DT Journal
LA English
AB A metabolic flux model was constructed for the yeast **Saccharomyces cerevisiae** comprising the most important reactions during anaerobic metab. of **xylose** and **glucose**. The model was used to calc. the intracellular fluxes in a recombinant, **xylose** -utilizing strain of **S. cerevisiae** (TMB 3001) grown anaerobically in a defined medium at diln. rates of 0.03, 0.06, and 0.18 h-1. The feed concn. was varied from 0 g/L **xylose** and 20 g/L **glucose** to a mixt. of 15 g/L **xylose** and 5 g/L **glucose**, so that the total concn. of carbon source was kept at 20 g/L. The specific uptake of **xylose** increased with the **xylose** concn. in the feed and with increasing diln. rate. The excreted xylitol was less than half of the **xylose** consumed. With increasing **xylose** concn. in the feed, the fluxes in the pentose phosphate pathway increased, whereas the flux through glycolysis decreased. Under all cultivation conditions, NAD (NADH) was the preferred cofactor for **xylose reductase**. The model showed that the flux through the reaction from ribulose 5-phosphate to xylulose 5-phosphate was very low under all cultivation conditions.
IT **50-99-7**, Dextrose, biological studies **58-86-6**, D-**Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(intracellular fluxes in a recombinant **xylose**-utilizing **Saccharomyces cerevisiae** cultivated anaerobically at different diln. rates and feed concns.)
IT **64-17-5**, **Ethanol**, biological studies
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(intracellular fluxes in a recombinant **xylose**-utilizing **Saccharomyces cerevisiae** cultivated anaerobically at different diln. rates and feed concns.)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
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Andreasen, A	1954	43	271	J Cell Comp Physiol	HCAPLUS
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Bruinenberg, P	1983	18	287	Eur J Appl Microbiol	HCAPLUS
Busturia, A	1986	132	379	J Gen Microbiol	HCAPLUS
Christensen, I	1995	50	2601	Chem Eng Sci	
Cirillo, V	1968	95	603	J Bacteriol	HCAPLUS
du Preez, J	1989	152	143	Arch Microbiol	HCAPLUS

Duboc, P	1995	43	145	J Biotechnol	HCAPLUS
Eliasson, A	2000	66	3381	Appl Environ Microbi	HCAPLUS
Herbert, D	1971	5B	209	Meth Microbiol	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ho, N	1989	11	417	Enzyme Microb Techno	HCAPLUS
Jones, E	1982		181	The molecular biolog	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Kotter, P	1990	18	493	Curr Genet	MEDLINE
Kotyk, A	1967	12	121	Folia Microbiol	HCAPLUS
Meinander, N	1996	142	165	Microbiology	HCAPLUS
Nielsen, J	1994		456	Bioreaction engineer	
Nissen, T	1997	143	203	Microbiology	HCAPLUS
Pronk, J	1996	12	1607	Yeast	HCAPLUS
Rizzi, M	1988	29	148	Appl Microbiol Biote	HCAPLUS
Rizzi, M	1989	67	20	J Ferment Bioeng	HCAPLUS
Roels, J	1983			Energetics and kinet	
Schulze, U	1995			thesis Technical uni	
Skoog, K	1990	56	3389	Appl Environ Microbi	HCAPLUS
Stephanopoulos, G	1998		725	Metabolic engineerin	
Stryer, L	1988			Biochemistry	
Tantirungkij, M	1993	75	83	J Ferment Bioeng	HCAPLUS
Umbarger, H	1978	47	533	Annu Rev Biochem	HCAPLUS
van Gulik, W	1995	48	681	Biotechnol Bioeng	HCAPLUS
van Zyl, C	1993	59	1487	Appl Environ Microbi	HCAPLUS
Vancauwenberge, J	1989	11	662	Enzyme Microb Techno	HCAPLUS
Vaseghi, S	1999	1	128	Metab Eng	HCAPLUS
Verduyn, C	1990	136	395	J Gen Microbiol	HCAPLUS
von Sivers, M	1995	51	43	Biores Technol	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 19 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:714529 HCAPLUS
DN 134:41163
TI Conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae** containing genes for **xylose reductase** and **xylitol dehydrogenase** from Pichia stipitis
AU Jin, Yong-Su; Lee, Tae-Hee; Choi, Yang-Do; Ryu, Yeon-Woo; Seo, Jin-Ho
CS Department of Food Science and Technology, Research Center for New Biomaterials in Agriculture, Seoul National University, Suwon, 441-744, S. Korea
SO Journal of Microbiology and Biotechnology (2000), 10(4), 564-567
CODEN: JOMBES; ISSN: 1017-7825
PB Korean Society for Applied Microbiology
DT Journal
LA English
AB A recombinant **Saccharomyces cerevisiae**, transformed with the genes encoding **xylose reductase** (XYL1) and **xylitol dehydrogenase** (XYL2) originated from Pichia stipitis CBS 5776, was developed to directly convert **xylose** to **ethanol**. A fed-batch fermn. with the recombinant yeast produced 8.7 g **ethanol**/l with a yield of 0.13 g **ethanol**/g **xylose** consumed.
IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae** contg. genes for **xylose reductase** and **xylitol dehydrogenase** from Pichia stipitis)
IT **58-86-6**, **Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae** contg. genes for **xylose reductase** and **xylitol dehydrogenase** from Pichia stipitis)

IT **9028-17-5, Xylitol dehydrogenase**
99775-25-4, Xylose reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(conversion of **xylose** to **ethanol** by recombinant **Saccharomyces cerevisiae** contg. genes for **xylose reductase** and **xylitol dehydrogenase** from Pichia stipitis)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Amore, R	1991	109	89	Gene	HCAPLUS
Bao, X	1997	13	225	Chin J Biotechnol	MEDLINE
Bothast, R	1999	15	867	Biotechnol Prog	HCAPLUS
Chandrakant, P	1998	18	295	Crit Rev Biotechnol	HCAPLUS
Cho, K	1999	9	340	J Microbiol Biotechn	HCAPLUS
Guebel, D	1991	7	287	J Ind Microbiol	HCAPLUS
Jeffries, T	1999	65	117	Adv Biochem Eng Biot	HCAPLUS
Koter, P	1993	38	776	Appl Microbiol Biote	
Koter, P	1990	18	493	Curr Genet	
Kweon, S	1993	8	452	Kor J Biotechnol Bio	
Pack, S	1998	8	441	J Microbiol Biotechn	HCAPLUS
Tantirungklj, M	1994	41	8	Appl Microbiol Biote	
van Zyl, W	1999	52	829	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 20 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:552809 HCAPLUS
DN 133:236908
TI Anaerobic **xylose** fermentation by recombinant **Saccharomyces cerevisiae** carrying XYL1, XYL2, and XKS1 in mineral medium chemostat cultures
AU Eliasson, Anna; Christensson, Camilla; Wahlbom, C. Fredrik; Hahn-Hagerdal, Barbel
CS Department of Applied Microbiology, Lund University, Lund, SE-221 00, Swed.
SO Applied and Environmental Microbiology (2000), 66(8), 3381-3386
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB For **ethanol** prodn. from lignocellulose, the fermn. of **xylose** is an economic necessity. **Saccharomyces cerevisiae** has been metabolically engineered with a **xylose** -utilizing pathway. However, the high **ethanol** yield and productivity seen with **glucose** have not yet been achieved. To quant. analyze metabolic fluxes in recombinant **S. cerevisiae** during metab. of **xylose-glucose** mixts., we constructed a stable **xylose**-utilizing recombinant strain, TMB 3001. The XYL1 and XYL2 genes from Pichia stipitis, encoding **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH), resp., and the endogenous XKS1 gene, encoding **xylulokinase** (XK), under control of the PGK1 promoter were integrated into the chromosomal HIS3 locus of **S. cerevisiae** CEN.PK 113-7A. The strain expressed XR, XDH, and XK activities of 0.4 to 0.5, 2.7 to 3.4, and 1.5 to 1.7 U/mg, resp., and was stable for more than 40 generations in continuous fermns. Anaerobic **ethanol** formation from **xylose** by recombinant **S. cerevisiae** was demonstrated for the first time. However, the strain grew on **xylose** only in the presence of oxygen.

Ethanol yields of 0.45 to 0.50 mmol of C/mmol of C (0.35 to 0.38 g/g) and productivities of 9.7 to 13.2 mmol of C h-1 g (dry wt.) of cells-1 (0.24 to 0.30 g h-1 g [dry wt.] of cells-1) were obtained from **xylose-glucose** mixts. in anaerobic chemostat cultures, with a diln. rate of 0.06 h-1. The anaerobic **ethanol** yield on **xylose** was estd. at 0.27 mol of C/(mol of C of **xylose**) (0.21 g/g), assuming a const. **ethanol** yield on **glucose** . The **xylose** uptake rate increased with increasing **xylose** concn. in the feed, from 3.3 mmol of C h-1 g (dry wt.) of cells-1 when the **xylose**-to-**glucose** ratio in the feed was 1:3 to 6.8 mmol of C h-1 g (dry wt.) of cells-1 when the feed ratio was 3:1. With a feed content of 15 g of **xylose**/L and 5 g of **glucose**/L, the **xylose** flux was 2.2 times lower than the **glucose** flux, indicating that transport limits the **xylose** flux.

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(anaerobic **xylose** fermn. by recombinant **Saccharomyces cerevisiae** carrying XYL1, XYL2, and XKS1 in mineral medium chemostat cultures)

IT **50-99-7**, Dextrose, biological studies **58-86-6**, D-**Xylose**, biological studies **9028-16-4, Xylitol dehydrogenase 9030-58-4, Xylulokinase 95829-40-6, Xylose reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(anaerobic **xylose** fermn. by recombinant **Saccharomyces cerevisiae** carrying XYL1, XYL2, and XKS1 in mineral medium chemostat cultures)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Andreasen, A	1953	41	23	J Cell Comp Physiol	HCAPLUS
Andreasen, A	1954	43	271	J Cell Comp Physiol	HCAPLUS
Anon	1974	1		Methods of enzymatic	
Berben, G	1991	7	475	Yeast	HCAPLUS
Boles, E	1993	9	761	Yeast	HCAPLUS
Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
Brooks, S	1988	255	R289	Am J Physiol	HCAPLUS
Bruinenberg, P	1983	18	287	Eur J Appl Microbiol	HCAPLUS
Busturia, A	1986	132	379	J Gen Microbiol	HCAPLUS
Chiang, C	1960	188	79	Nature	HCAPLUS
Christensen, I	1995	50	2601	Chem Eng Sci	
Ciriacy, M	1986		675	Biomolecular enginee	
de Jong-Gubbels, P	1995	11	407	Yeast	HCAPLUS
Deng, X	1990	24/25	193	Appl Biochem Biotech	
Dobson, M	1980	2	193	Curr Genet	HCAPLUS
Duboc, P	1995	43	145	J Biotechnol	HCAPLUS
Eliasson, A	2000	53	376	Appl Microbiol Biote	HCAPLUS
Entian, K	1998	26	431	Yeast gene analysis	HCAPLUS
Futcher, A	1984	157	283	J Bacteriol	HCAPLUS
Hahn-Hagerdal, B	1996	782	286	Ann N Y Acad Sci	MEDLINE
Ho, N	1997			WO 97/42307	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Hochster, R	1954	48	120	Arch Biochem	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Kotyk, A	1967	12	121	Folia Microbiol	HCAPLUS
Mason, C	1991	59	269	Antonie Leeuwenhoek	HCAPLUS
Meinander, N	1999	68	79	Bioresour Technol	HCAPLUS
Meinander, N	1997	54	391	Biotechnol Bioeng	HCAPLUS
Muller, S	1995	177	4517	J Bacteriol	MEDLINE

Nagy, M	1992	89	8966	Proc Natl Acad Sci U	HCAPLUS
Olsson, L	1994	16	388	Enzyme Microb Techno	HCAPLUS
Rizzi, M	1988	29	148	Appl Microbiol Biote	HCAPLUS
Rizzi, M	1989	67	20	J Ferment Bioeng	HCAPLUS
Roels, J	1983			Energetics and kinet	
Sambrook, J	1989			Molecular cloning: a	
Scherer, S	1979	76	4951	Proc Natl Acad Sci U	HCAPLUS
Schiestl, R	1989	16	339	Curr Genet	HCAPLUS
Senac, T	1990	56	120	Appl Environ Microbi	HCAPLUS
Shamanna, D	1979	139	64	J Bacteriol	HCAPLUS
Sherman, F	1991	194	3	Methods Enzymol	HCAPLUS
Shi, N	1998	50	339	Appl Microbiol Biote	HCAPLUS
Skoog, K	1990	56	3389	Appl Environ Microbi	HCAPLUS
Snoep, J	1995	141	2329	Microbiology	HCAPLUS
Tantirungkij, M	1993	75	83	J Ferment Bioeng	HCAPLUS
Toon, S	1997	63-65	243	Appl Biochem Biotech	HCAPLUS
van Dijken, J	1986	32	199	FEMS Microbiol Rev	HCAPLUS
Verduyn, C	1985	226	669	Biochem J	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Visser, W	1990	56	3785	Appl Environ Microbi	HCAPLUS
von Sivers, M	1995	51	43	Bioresour Technol	HCAPLUS
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1996	62	4648	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 21 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:521143 HCAPLUS
DN 133:206810
TI Characterization of two-substrate fermentation processes for xylitol production using recombinant **Saccharomyces cerevisiae** containing **xylose reductase** gene
AU Lee, Woo-Jong; Ryu, Yeon-Woo; Seo, Jin-Ho
CS Department of Food Science and Technology, Research Center for New Bio-Materials in Agriculture, Seoul National University, Suwon, 441-744, S. Korea
SO Process Biochemistry (Oxford) (2000), 35(10), 1199-1203
CODEN: PBCHE5; ISSN: 1359-5113
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Fermn. characteristics of recombinant **Saccharomyces cerevisiae** contg. a **xylose reductase** gene from Pichia stipitis were investigated in an attempt to convert **xylose** to xylitol, a natural five-carbon sugar alc. used as a sweetener. Xylitol was produced with a max. yield of 0.95 g g-1 xylitol **xylose** consumed in the presence of **glucose** used as a co-substrate for co-factor regeneration. Addn. of **glucose** caused inhibition of **xylose** transport and accumulation of **ethanol**. Such problems were solved by adopting **glucose**-limited fed-batch fermns. where a high ratio of **xylose** to **glucose** was maintained during the bioconversion phase. The optimized two-substrate fed-batch fermn. carried out with **S. cerevisiae** EH13.15:pY2XR at 30.degree.C resulted in 105.2 g l-1 xylitol concn. with 1.69 g l-1 h-1 productivity.
IT **50-99-7**, D-**Glucose**, biological studies **58-86-6**, D-**Xylose**, biological studies **99775-25-4**, **Xylose reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(two-substrate fermn. processes for xylitol prodn. using recombinant **Saccharomyces cerevisiae** contg. **xylose reductase** gene)
IT **64-17-5**, **Ethanol**, biological studies

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(two-substrate fermn. processes for xylitol prodn. using recombinant **Saccharomyces cerevisiae** contg. **xylose reductase** gene)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Choi, C	1996	18	1129	Biotechnol Lett	HCAPLUS
Cillilo, V	1968	95	603	J Gen Bacteriol	
Deis, R	1993		94	Food Technol	
Dieters, W	1975			CH 560175	HCAPLUS
Hallborn, J	1991	9	1090	Biotechnol	HCAPLUS
Hyvonen, L	1983	28	373	Adv Food Res	
Kim, J	1999	22	181	J Ind Microbiol Biot	HCAPLUS
Kotyk, A	1967	12	121	Fol Microbiol	HCAPLUS
Melaja, A	1977			US 4008285	HCAPLUS
Nigam, P	1995	30	117	Process Biochem	HCAPLUS
O'Connor, G	1992	39	293	Biotech Bioeng	HCAPLUS
Pepper, T	1988	10	98	Food Technol	
Rieger, M	1983	129	653	J Gen Microbiol	HCAPLUS
van Zyl, C	1993	59	1487	Appl Environ Microbi	HCAPLUS
van Zyl, C	1989	135	2791	J Gen Microbiol	HCAPLUS
Washuttl, J	1973	38	1262	J Food Sci	

L71 ANSWER 22 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 2000:291166 HCAPLUS
DN 133:57615
TI Xylulose fermentation by mutant and wild-type strains of Zygosaccharomyces and **Saccharomyces cerevisiae**
AU Eliasson, A.; Boles, E.; Johansson, B.; Osterberg, M.; Thevelein, J. M.; Spencer-Martins, I.; Juhnke, H.; Hahn-Hagerdal, B.
CS Department of Applied Microbiology, Lund University, Lund, SE-221 00, Swed.
SO Applied Microbiology and Biotechnology (2000), 53(4), 376-382
CODEN: AMBIDG; ISSN: 0175-7598
PB Springer-Verlag
DT Journal
LA English
AB Anaerobic xylulose fermn. was compared in strains of Zygosaccharomyces and **Saccharomyces cerevisiae**, mutants and wild-type strains to identify host-strain background and genetic modifications beneficial to **xylose** fermn. Overexpression of the gene (XKS1) for the pentose phosphate pathway (PPP) enzyme **xylulokinase** (XK) increased the **ethanol** yield by almost 85% and resulted in **ethanol** yields [0.61 C-mmol (C-mmol consumed xylulose)-1] that were close to the theor. yield [0.67 C-mmol (C-mmol consumed xylulose)-1]. Likewise, deletion of gluconate 6-phosphate dehydrogenase (gnd1.DELTA.) in the PPP and deletion of trehalose 6-phosphate synthase (tps1.DELTA.) together with trehalose 6-phosphate phosphatase (tps2.DELTA.) increased the **ethanol** yield by 30% and 20%, resp. Strains deleted in the promoter of the phosphoglucose isomerase gene (PGI1) - resulting in reduced enzyme activities - increased the **ethanol** yield by 15%. Deletion of ribulose 5-phosphate epimerase (rpe1.DELTA.) in the PPP abolished **ethanol** formation completely. Among nontransformed and parental strains **S. cerevisiae** ENY.WA-1A exhibited the highest **ethanol** yield, 0.47 C-mmol (C-mmol consumed xylulose)-1. Other nontransformed strains produced mainly arabinitol or xylitol from xylulose under anaerobic conditions. Contrary to previous reports **S. cerevisiae** T23D and CBS 8066 were not isogenic with respect to pentose metab. Whereas, CBS 8066 has been reported to have a high **ethanol** yield on xylulose, 0.46 C-mmol

(C-mmol consumed xylulose)-1 (Yu et al. 1995), T23D only formed **ethanol** with a yield of 0.24 C-mmol (C-mmol consumed xylulose)-1. Strains producing arabinitol did not produce xylitol and vice versa. However, overexpression of XKS1 shifted polyol formation from xylitol to arabinitol.

IT **64-17-5P, Ethanol**, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(xylulose fermn. by mutant and wild-type strains of Zygosaccharomyces and **Saccharomyces cerevisiae**)

IT **9030-58-4, Xylulokinase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(xylulose fermn. by mutant and wild-type strains of Zygosaccharomyces and **Saccharomyces cerevisiae**)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Anon	1991	194		Guide to yeast genet	
Boles, E	1994	243	363	Mol Gen Genet	MEDLINE
Boles, E	1993	9	761	Yeast	HCAPLUS
Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
Brown, A	1990			Microbial water stre	
Bruinenberg, P	1983	18	287	Eur J Appl Microbiol	HCAPLUS
De Jong-Gubbels, P	1995	11	407	Yeast	HCAPLUS
Deng, X	1990	24/25	193	Appl Biochem Biotech	
Gietz, R	1988	74	527	Gene	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Ho, N	1993			US5789210	
Hohmann, S	1996	20	981	Mol Microbiol	HCAPLUS
Jeppsson, H	1995	61	2596	Appl Environ Microbi	HCAPLUS
Jeppsson, H	1996	62	1705	Appl Environ Microbi	HCAPLUS
Johansson, B				submitted for public	
Juhnke, H	1996	252	456	Mol Gen Genet	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Maitra, P	1971	246	475	J Biol Chem	HCAPLUS
Mellor, J	1983	24	1	Gene	HCAPLUS
Miosga, T	1996	30	404	Curr Genet	HCAPLUS
Muller, S	1995	177	4517	J Bacteriol	MEDLINE
Neves, M	1995	27	110	Curr Genet	HCAPLUS
Olsson, L	1994	16	388	Enzyme Microb Techno	HCAPLUS
Olsson, L	1996	18	312	Enzyme Microb Techno	HCAPLUS
Pronk, J	1994	140	601	Microbiology	HCAPLUS
Rodrigues de Sousa, H	1995	18	44	Syst Appl Microbiol	HCAPLUS
Rodriguez-Pena, J	1998	162	155	FEMS Microbiol Lett	HCAPLUS
Rose, M	1991	199	511	Eur J Biochem	HCAPLUS
Sambrook, J	1989			Molecular cloning: a	
Schiestl, R	1989	16	339	Curr Genet	HCAPLUS
Senac, T	1990	56	120	Appl Environ Microbi	HCAPLUS
Shamanna, D	1979	139	64	J Bacteriol	HCAPLUS
Sikorski, R	1989	122	19	Genetics	HCAPLUS
Sousa, M	1996	62	3152	Appl Environ Microbi	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Microbiol Biote	HCAPLUS
Thomas, B	1989	56	619	Cell	HCAPLUS
Thomas, D	1985	2	157	Food Microbiol	
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Wenzel, T	1992	209	697	Eur J Biochem	HCAPLUS
Yu, S	1995	44	314	Appl Microbiol Biote	HCAPLUS
Zamenhoff, S	1957	3	696	Methods Enzymol	

L71 ANSWER 23 OF 29 HCAPLUS COPYRIGHT 2003 ACS

AN 1999:813129 HCAPLUS
DN 132:150648
TI **Xylose** utilization by recombinant strains of **Saccharomyces cerevisiae** on different carbon sources
AU Van Zyl, W. H.; Eliasson, A.; Hobley, T.; Hahn-Hagerdal, B.
CS Department of Microbiology, University of Stellenbosch, Stellenbosch, 7600, S. Afr.
SO Applied Microbiology and Biotechnology (1999), 52(6), 829-833
CODEN: AMBIDG; ISSN: 0175-7598
PB Springer-Verlag
DT Journal
LA English
AB Autoselective **xylose**-utilizing strains of **S. cerevisiae** expressing the **xylose reductase** (XYL1) and **xylitol dehydrogenase** (XYL2) genes of Pichia stipitis were constructed by replacing the chromosomal FUR1 gene with a disrupted fur1::LEU2 allele. Anaerobic fermns. with 80 g/L D-**xylose** as substrate showed a 2-fold higher consumption of **xylose** in complex medium than in defined medium. The **xylose** consumption rate increased a further 3-fold when 20 g/L D-**glucose** or raffinose was used as co-substrate together with 50 g/L D-**xylose**. **Xylose** consumption was higher with raffinose as co-substrate than with **glucose** (85% vs. 71%, resp.) after 82-h fermns. A high initial **EtOH** concn. and moderate levels of glycerol and HOAc accompanied **glucose** as co-substrate, whereas the **EtOH** concn. gradually increased with raffinose as co-substrate with no glycerol and much less HOAc formation.
IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(fermn.; **xylose** utilization by recombinant strains of **Saccharomyces cerevisiae** on different carbon sources)
IT **50-99-7**, D-**Glucose**, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(**xylose** utilization by recombinant strains of **Saccharomyces cerevisiae** on different carbon sources)
IT **58-86-6**, D-**Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(**xylose** utilization by recombinant strains of **Saccharomyces cerevisiae** on different carbon sources)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Boles, E	1997	21	85	FEMS Microbiol Rev	HCAPLUS
Busturia, A	1986	132	379	J Gen Microbiol	HCAPLUS
Chiang, L	1981	42	284	Appl Environ Microbi	HCAPLUS
Gancedo, C	1989	3	205	metabolism and physi	
Gancedo, J	1998	62	334	Microbiol Mol Biol R	HCAPLUS
Gasent-Ramirez, J	1995	61	2113	Appl Environ Microbi	MEDLINE
Hahn-Hagerdal, B	1993		231	Bioconversion of for	
Heredia, C	1968	5	321	Eur J Biochem	HCAPLUS
Hill, J	1991	19	5791	Nucleic Acids Res	HCAPLUS
Ho, N	1998	64	1852	Appl Environ Microbi	MEDLINE
Jeffries, T	1990		349	Yeast: biotechnology	HCAPLUS
Kotyk, A	1967	10	121	Properties of the su	
La Grange, D	1996	62	1036	Appl Environ Microbi	HCAPLUS
Liang, H	1996	7	1953	Mol Biol Cell	HCAPLUS
Loison, G	1986	4	433	Bio/Technology	HCAPLUS
Meinander, N	1997	63	1959	Appl Environ Microbi	HCAPLUS

Meinander, N	1996	142	165	Microbiology	HCAPLUS
Ozcan, S	1996	93	12428	Proc Natl Acad Sci	MEDLINE
Reifenberger, E	1997	245	324	Eur J Biochem	HCAPLUS
Rothstein, R	1983	101	202	Methods Enzymol	HCAPLUS
Sambrook, J	1989			Molecular cloning: a	
Senac, T	1990	56	120	Appl Environ Microbi	HCAPLUS
Serraro, R	1974	5	161	Mol Celi Biochem	
Thestrup, H	1995	61	2043	Appl Environ Microbi	HCAPLUS
Van Zyl, C	1993	59	1487	Appl Environ Microbi	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Wang, P	1980	26	1165	Can J Microbiol	HCAPLUS
Yu, S	1995	44	314	Appl Microbiol Biote	HCAPLUS

L71 ANSWER 24 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:700162 HCAPLUS
DN 132:261187
TI Construction of recombinant **S. cerevisiae** harboring both **xylose reductase** and **xylitol dehydrogenase** genes
AU Wang, Tianhong; Penttila, Merja; Li, Bo
CS National Key Laboratory of Microbial Technology, Shandong University, Jinan, 250100, Peop. Rep. China
SO Junwu Xitong (1999), 18(3), 311-315
CODEN: JUXIFB; ISSN: 1007-3515
PB Kexue Chubanshe
DT Journal
LA Chinese
AB The recombinant **S. cerevisiae** strain HX1 harboring both xr from Pichia stipitis and xdh1 from Trichoderma reesei were constructed by transformation of plasmid pAJ401-xdh1 harboring T. reesei xdh gene into recombinant **S. cerevisiae** strain H475 harboring P. stipitis xr gene by using two vectors-system. The utilization and conversion of **xylose** by this recombinant strain HX1 were studied. The strain HX1 was able to grow on the medium with **xylose** as the sole carbon source. **S. cerevisiae** HX1 was able to convert more than 90% of the **xylose** into xylitol, **ethanol** and other products when grew in 1.8% **xylose** in shake flasks at 30.degree.. The conversion efficiency of **xylose** into xylitol was 56-66% and 0.9 g L-1 **ethanol** prodn. was obtained. The situations of HX1 grown on the medium in which 1.8% **xylose** + 0.2% **glucose** as carbon sources were studied also.
IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(construction of recombinant **Saccharomyces cerevisiae** harboring the **xylose reductase** gene from Pichia stipitis and **xylitol dehydrogenase** gene from Trichoderma reesei and utilization and conversion of **xylose** by recombinant strain HX1)
IT **9028-16-4, Xylitol dehydrogenase**
99775-25-4, Xylose reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(construction of recombinant **Saccharomyces cerevisiae** harboring the **xylose reductase** gene from Pichia stipitis and **xylitol dehydrogenase** gene from Trichoderma reesei and utilization and conversion of **xylose** by recombinant strain HX1)

L71 ANSWER 25 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:691222 HCAPLUS
DN 131:332982

TI Genetically engineered yeast and mutants thereof for the efficient fermentation of lignocellulose hydrolysates to **ethanol**

IN Traff, Karin L.; Cordero Otero, Ricardo Roman; Van Zyl, Wilem Heber; Hahn-Hagerdal, Barbel

PA Forskarpatent i Syd AB, Swed.

SO PCT Int. Appl., 29 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9954477	A2	19991028	WO 1999-IB1046	19990420
	WO 9954477	A3	19991202		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9939507	A1	19991108	AU 1999-39507	19990420
	EP 1071786	A2	20010131	EP 1999-922422	19990420
	R: DE, FR, GB, IT, SE				
	JP 2002512037	T2	20020423	JP 2000-544808	19990420
	US 6410302	B1	20020625	US 1999-294894	19990420
PRAI	US 1998-82334P	P	19980420		
	WO 1999-IB1046	W	19990420		

AB The present invention provides genetically engineered expression vectors, and recombinant yeast strains comprising those vectors, or portions of those vectors. The vectors comprise a modified form of a gene encoding an aldose reductase (AR) enzyme in which only a portion of the gene is present on the vector. Preferably the vectors comprise the flanking sequences taken from one or both ends of the AR-encoding gene. The vectors are used to delete or disrupt the AR-encoding gene of a host cell, and the recombinant cells made in this manner are capable of fermenting lignocellulose and/or lignocellulose hydrolyzates to **ethanol** in high quantities. The vector of the invention also permits any heterologous sequence to be integrated into the host genomic AR sequence, esp. one encoding a **xylose**-utilizing enzyme. In particular, the invention relates to the use of a provided vector in engineering a yeast strain that shows enhanced conversion of **xylose** to **ethanol** while simultaneously showing reduced xylitol formation.

IT **249571-96-8P**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(amino acid sequence; genetically engineering yeasts to efficiently degrade **xylose** to **ethanol** while simultaneously showing reduced xylitol formation)

IT **58-86-6, Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); REM (Removal or disposal); BIOL (Biological study); PROC (Process)
(degrdn. of; vectors comprising portions of an aldose reductase gene and uses thereof in genetically engineering yeasts to efficiently degrade **xylose** to **ethanol**)

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermn.; vectors comprising portions of an aldose reductase gene and uses thereof in genetically engineering yeasts to efficiently degrade

lignocellulose hydrolyzates to **ethanol**)

IT **9028-31-3**, Aldose reductase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene encoding; vectors comprising portions of an aldose reductase gene and uses thereof in genetically engineering yeasts to efficiently degrade lignocellulose hydrolyzates to **ethanol**)

IT **64-17-5P**, **Ethanol**, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(vectors comprising portions of an aldose reductase gene and uses thereof in genetically engineering yeasts to efficiently degrade lignocellulose hydrolyzates to **ethanol**)

L71 ANSWER 26 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:595342 HCAPLUS
DN 131:227744
TI Improving fermentation yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes
IN Aristidou, Aristos; Londesborough, John; Penttila, Merja; Richard, Peter; Ruohonen, Laura; Soderlund, Hans; Teleman, Anita; Toivari, Mervi
PA Valtion Teknillinen Tutkimuskeskus, Finland
SO PCT Int. Appl., 93 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9946363	A1	19990916	WO 1999-FI185	19990311
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	FI 9800551	A	19990912	FI 1998-551	19980311
	AU 9927303	A1	19990927	AU 1999-27303	19990311
	EP 981600	A1	20000301	EP 1999-907641	19990311
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2001525682	T2	20011211	JP 1999-545439	19990311
PRAI	FI 1998-551	A	19980311		
	WO 1999-FI185	W	19990311		

AB A method of increasing the productivity of fermentor microorganisms by increasing the electron flow between NAD/NADH and NADP/NADPH using dehydrogenases is described. The microorganisms are transformed with the genes for one or more enzymes that functionally couple the oxidn. and redn. of substrates by two pyridine nucleotide-linked dehydrogenase reactions with different specificities for the NAD/NADH and NADP/NADPH coenzyme couples and so facilitates the transfer of electrons between the two coenzyme couples through the substrates. In particular the invention relates to increasing the yields of products such as **ethanol** or amino acids from carbon and nitrogen sources such as biomass comprising hexoses, pentoses or their polymers. A **xylose**-utilizing redox couple using the enzymes **xylose reductase**, **xylitol dehydrogenase**, **xylulokinase**, and NAD-dependent glutamate dehydrogenase was constructed in Pichia (Yamadazyma) stipitis using the strong PGK1 and ADH1 promoters. The transgenic cells with the novel redox system utilized **xylose** to yield **ethanol** at 2.35 g **ethanol**/g dry wt. compared to

1.47 g **ethanol**/g dry wt. for control cells after two days at 30.degree. in a defined medium D-**xylose** at 20 g/L.

IT **58-86-6**, **Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(as electron carrier in enzymic redox system; improving fermn. yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes)

IT **50-99-7**, D-**Glucose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**ethanol** fermn. from; improving fermn. yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes)

IT **64-17-5P**, **Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermn. of; improving fermn. yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes)

IT **9030-58-4**, **Xylulokinase**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(gene for, of **Saccharomyces cerevisiae**, cloning and expression of; improving fermn. yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes)

IT **53-57-6**, NADPH **53-59-8**, NADP **53-84-9**, NAD
58-68-4, NADH
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(improving fermn. yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes)

IT **9028-16-4**, **Xylitol dehydrogenase**
104118-53-8, **Xylose reductase**
RL: BPR (Biological process); BSU (Biological study, unclassified); CAT (Catalyst use); BIOL (Biological study); PROC (Process); USES (Uses)
(redox system using; improving fermn. yields from biomass using microorganisms with improved electron transfer between nicotinamide coenzymes)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Ajinomoto Co, Inc	1996			EP 0733712 A1	HCAPLUS
Meinander, N	1996	142	165	Microbiology	HCAPLUS
Purdue Research Foundat	1997			WO 9742307 A1	HCAPLUS

L71 ANSWER 27 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 1999:105885 HCAPLUS
DN 130:222204
TI Fermentation of **xylose/glucose** mixtures by metabolically engineered **Saccharomyces cerevisiae** strains expressing XYL1 and XYL2 from Pichia stipitis with and without overexpression of TAL1
AU Meinander, Nina Q.; Boels, Ingeborg; Hahn-Hagerdal, Barbel
CS Applied Microbiology, Lund Institute of Technology/University of Lund, Lund, S-221 00, Swed.
SO Bioresource Technology (1998), Volume Date 1999, 68(1), 79-87
CODEN: BIRTEB; ISSN: 0960-8524
PB Elsevier Science Ltd.
DT Journal
LA English
AB Anaerobic **xylose** conversion by two metabolically engineered

Saccharomyces cerevisiae strains in the presence and absence of simultaneous **glucose** metab. was investigated. One strain expressed XYL1 encoding **xylose reductase** (XR) and XYL2 encoding **xylitol dehydrogenase** (XDH) from Pichia stipitis, whereas the other addnl. overexpressed TAL1 encoding transaldolase (TAL). Both strains formed xylitol as the main product of **xylose** metab. The TAL1-overexpressing strain gave a higher biomass yield and produced less carbon dioxide and somewhat less xylitol compared with the XYL1 + XYL2 strain, indicating that TAL limited **xylose** metab. in the latter. The **ethanol** yield was similar with both strains. The simultaneous metab. of **glucose** enhanced **xylose** metab. by causing a higher rate of **xylose** consumption and less xylitol and xylulose excretion, compared with **xylose** metab. alone. Simultaneous **xylose** and **glucose** metab. affected the growth rate neg. compared with growth on **glucose** alone. Addnl., comparison of the specific growth rate of the host strain, a ref. strain with a plasmid without XYL1, XYL2 or TAL1, the XYL1+XYL2 strain and the XYL1 + XYL2 + TAL1 strain on **glucose**, showed that the presence of plasmids and expression of genes on the plasmids caused a decrease in specific growth rates related to the no. of plasmids present and the no. of structural genes on the plasmids. Both strains exhibited high XR and XDH activities in batch cultivation, but rapidly lost the activities in chemostat cultivation. Limitations in the **xylose**-metabolizing pathway and further improvement of recombinant **xylose**-metabolizing **S. cerevisiae** are discussed.

IT **64-17-5P, Ethanol**, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermentation; fermn. of **xylose/glucose** mixts. by metabolically engineered **Saccharomyces cerevisiae** expressing genes XYL1 and XYL2 from Pichia stipitis with and without overexpression of gene TAL1)

IT **9028-16-4, Xylitol dehydrogenase**
9028-31-3, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(fermn. of **xylose/glucose** mixts. by metabolically engineered **Saccharomyces cerevisiae** expressing genes XYL1 and XYL2 from Pichia stipitis with and without overexpression of gene TAL1)

IT **64-17-5P, Ethanol**, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(fermn. of **xylose/glucose** mixts. by metabolically engineered **Saccharomyces cerevisiae** expressing genes XYL1 and XYL2 from Pichia stipitis with and without overexpression of gene TAL1)

IT **50-99-7**, D-**Glucose**, biological studies **58-86-6**, D-**Xylose**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(fermn. of **xylose/glucose** mixts. by metabolically engineered **Saccharomyces cerevisiae** expressing genes XYL1 and XYL2 from Pichia stipitis with and without overexpression of gene TAL1)

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Bjorling, T	1989	11	240	Enzyme Microb Techno	
Boles, E	1996	19	639	Mol Microbiol	
Boles, E	1993	9	761	Yeast	HCAPLUS

Bradford, M	1976	72	248	Anal Biochem	HCAPLUS
Bruinenberg, P	1984	19	256	Appl Microbiol Biote	HCAPLUS
Bruinenberg, P	1983	129	965	J Gen Microbiol	HCAPLUS
Busturia, A	1986	132	379	J Gen Microbiol	HCAPLUS
Deng, X	1990	24/25	193	Appl Biotechnol Bioc	
Fein, J	1984	30	682	Can J Microbiol	HCAPLUS
Gancedo, C	1967	26	528	Biochim Biophys Res	HCAPLUS
Gopal, C	1989	30	160	Appl Microbiol Biote	HCAPLUS
Hahn-Hagerdal, B	1996	782	286	Annals of the New Yo	MEDLINE
Hahn-Hagerdal, B	1994	41	62	Appl Microbiol Biote	
Hayn, M	1993		33	Bioconversion of For	HCAPLUS
Hinman, N	1989	20/21	391	Appl Biotechnol Bioc	
Ho, N	1994			WO 9513362	HCAPLUS
Janes, M	1990	18	97	Curr Genet	HCAPLUS
Kotter, P	1993	38	776	Appl Microbiol Biote	
Kotter, P	1990	18	493	Curr Genet	MEDLINE
Leao, C	1982	24	2601	Biotechnol Bioeng	HCAPLUS
Ligthelm, M	1988	28	63	Appl Microbiol Biote	HCAPLUS
Linden, T	1989	3	189	Biotechnol Tech	HCAPLUS
Lohmeier-Vogel, E	1995	61	1414	Appl Environ Microbi	HCAPLUS
Meinander, N	1997	63	1959	Appl Environ Microbi	HCAPLUS
Meinander, N	1997	54	391	Biotechnol Bioeng	HCAPLUS
Meinander, N	1996	142	165	Microbiol	HCAPLUS
Meinander, N	1994	9	1143	Progress in Biotrchn	HCAPLUS
Mellor, J	1983	24	1	Gene	HCAPLUS
Muller, S	1995	177	4517	J Bacteriol	MEDLINE
Olsson, L	1992	34/35	359	Appl Biotechnol Bioc	
Olsson, L	1993	28	249	Process Biochem	HCAPLUS
Roels, J	1983			Energetics and Kinet	
Sanchez, B	1988	10	315	Enzyme Microb Techno	HCAPLUS
Schaaff-Gerstenschlager	1994	50	59	Biores Technol	
Senac, T	1990	56	120	Appl Environ Microbi	HCAPLUS
Seo, J	1985	27	1668	Biotechnol Bioeng	HCAPLUS
Skoog, K	1992	34/35	369	Appl Biotechnol Bioc	
Skoog, K	1990	56	3389	Appl Environ Microbi	HCAPLUS
Tantirungkij, M	1994	41	8	Appl Microbiol Biote	HCAPLUS
Tantirungkij, M	1993	75	83	J Ferm Biotechnol	HCAPLUS
Tran, A	1986	8	439	Enzyme Microb Techno	HCAPLUS
van Zyl, C	1993	59	1487	Appl Environ Microbi	HCAPLUS
van Zyl, C	1991	13	82	Enzyme Microb Techno	HCAPLUS
van Zyl, C	1989	135	2791	J Gen Microbiol	HCAPLUS
van der Aar, P	1990	32	577	Appl Microbiol Biote	HCAPLUS
Verduyn, C	1992	8	501	Yeast	HCAPLUS
Walfridsson, M	1995	61	4184	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1996	62	4648	Appl Environ Microbi	HCAPLUS
Walfridsson, M	1997	48	218	Appl Microbiol Biote	HCAPLUS
Watson, N	1984	6	447	Enzyme Microb Techno	HCAPLUS
Watson, N	1984	6	451	Enzyme Microb Techno	HCAPLUS
Wright, J	1988	84	62	Chem Eng Prog	HCAPLUS

L71 ANSWER 28 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 1998:748524 HCAPLUS
DN 130:134664
TI Isolation and identification of **xylitol dehydrogenase** gene from Trichoderma reesei
AU Wang, Tianhong; Penttila, Merja; Gao, Peiji; Wang, Chunhui; Zhong, Ling
CS Natl. Key Lab. Microbial Technol., Shandong Univ., Jinan, 250100, Peop. Rep. China
SO Shengwu Gongcheng Xuebao (1998), 14(3), 320-325
CODEN: SGXUED; ISSN: 1000-3061
PB Kexue Chubanshe
DT Journal
LA Chinese

AB A cDNA sub-library from the fungus Trichoderma reesei grown on xylan was constructed in **S. cerevisiae** recombinant strain H475 harboring **xylose reductase** (XR) gene from Pichia stipitis. The sub-library was screened for **xylitol dehydrogenase** (XDH) gene on SC selective medium in which **xylose** was used as a sole carbon source. The XDH gene, xdhl, was isolated from this sub-pool and the length of xdhl is about 1.3 kb. The mol. wt. of the **xylitol dehydrogenase** produced by **S. cerevisiae** recombinant strain HX1 is about 40 kDa. The strain of HX1 harboring both **xylose reductase** from P. stipitis and xdhl from T. ressei was able to grown on xylase medium and converted more than 90% at the **xylose** into xylitol, **ethanol** and another byproduct.

IT **9028-16-4P**
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(cloning and expression of **xylitol dehydrogenase** gene from Trichoderma reesei)

L71 ANSWER 29 OF 29 HCAPLUS COPYRIGHT 2003 ACS
AN 1993:424409 HCAPLUS
DN 119:24409
TI Role of D-ribose as a cometabolite in D-**xylose** metabolism by **Saccharomyces cerevisiae**
AU van Zyl, Carina; Prior, Bernard A.; Kilian, Stephanus G.; Brandt, E. Vincent
CS Dep. Microbiol. Biochem., Univ. Orange Free State, Bloemfontein, 9300, S. Afr.
SO Applied and Environmental Microbiology (**1993**), 59(5), 1487-94
CODEN: AEMIDF; ISSN: 0099-2240
DT Journal
LA English
AB The influence of D-ribose as a cosubstrate on the uptake and metab. of the non-growth substrate D-**xylose** by **S. cerevisiae** ATCC 26602 was investigated. **Xylose** was taken up by means of low- and high-affinity **glucose** transport systems. In cells exposed for 2 days to a mixt. of **xylose** and ribose, only the high-affinity system could be detected. **Glucose** strongly inhibited the transport of **xylose** by both systems. Starvation or exposure to either **xylose** or ribose resulted in inactivation of **xylose** transport, which did not occur in the presence of a mixt. of ribose and **xylose**. A constitutive non-**glucose** -repressible NADPH2-dependent **xylose reductase** with a specific activity of .apprx.5 mU/mg of protein that converted **xylose** to xylitol was present in a **glucose**-grown culture. No activity converting xylitol to xylulose or vice versa was found in crude exts. Both **xylose** and ribose were converted to their corresponding polyols, xylitol and ribitol, as indicated by 13C-NMR spectroscopy. Furthermore, **ethanol** was detected, and this implied that pathways for the complete catabolism of **xylose** and ribose exist. However, the NADPH2 required for the conversion of **xylose** to xylitol is apparently not supplied by the pentose phosphate pathway since the **ethanol** produced from D-[1-13C] **xylose** was labeled only in the C-2 position. Acetic acid was produced from ribose and may assist in the conversion of **xylose** to xylitol by cycling NADPH2.

IT **58-86-6, D-Xylose,** biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of, by **Saccharomyces cerevisiae**)

IT **95829-40-6, Xylose reductase**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence)

(of **Saccharomyces cerevisiae**)
IT **50-99-7**, D-**Glucose**, biological studies
RL: BIOL (Biological study)
(**xylose** metab. by **Saccharomyces cerevisiae** in relation to)

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FILE 'BIOSIS' ENTERED AT 07:41:05 ON 18 MAR 2003

FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 12 March 2003 (20030312/ED)

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L131 ANSWER 1 OF 20 BIOSIS
AN 1996:354302 BIOSIS
DN PREV199699076658
TI Redox balances in recombinant **Saccharomyces cerevisiae**
.
AU Hahn-Hagerdal, Barbel (1); Hallborn, Johan (1); Jeppsson, Helena (1); Meinander, Nina (1); Walfridsson, Mats (1); Ojamo, Heikki; Penttila, Merja; Zimmermann, Friedrich K.
CS (1) Dep. Appl. Microbiol., Lund Univ., P.O. Box 124, S-221 00 Lund Sweden
SO Asenjo, J. A. [Editor]; Andrews, B. A. [Editor]. Annals of the New York Academy of Sciences, (1996) Vol. 782, pp. 286-296. Annals of the New York Academy of Sciences; Recombinant DNA biotechnology, III. The integration of biological and engineering sciences.
Publisher: New York Academy of Sciences 2 East 63rd Street, New York, New York 10021, USA.
Meeting Info.: Conference Deauville, France October 16-21, 1994
ISSN: 0077-8923. ISBN: 0-89766-962-2 (paper), 0-89766-961-4 (cloth).
DT Book; Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Food Technology - General; Methods *13502
Food Technology - Sugar *13524
Food Technology - Evaluations of Physical and Chemical Properties *13530
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
BC **Ascomycetes *15100**
IT Major Concepts
Bioprocess Engineering; Foods; Genetics; Metabolism
IT Chemicals & Biochemicals
XYLOSE REDUCTASE; **XYLITOL DEHYDROGENASE**; TRANSKETOLASE; TRANSALDOLASE; **XYLOSE**; **ETHANOL**; XYLITOL; **GLUCOSE**
IT Miscellaneous Descriptors
ARTIFICIAL SWEETENER; BIOPROCESS ENGINEERING; BOOK CHAPTER; **ETHANOL**; FERMENTATION; **GLUCOSE**; MEETING PAPER; PRODUCTION; RECOMBINANT PRODUCER ORGANISM; REDOX BALANCE; SOURCE ORGANISM; STRAIN-H474; STRAIN-H550; STRAIN-S104; STRAIN-S641; TRANSALDOLASE; TRANSKETOLASE; UTILIZATION; XYLITOL; **XYLITOL DEHYDROGENASE**; **XYLOSE**; **XYLOSE**

REDUCTASE
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **95829-40-6Q (XYLOSE REDUCTASE)**
99775-25-4Q (XYLOSE REDUCTASE)
104118-53-8Q (XYLOSE REDUCTASE)
9028-16-4Q (XYLITOL DEHYDROGENASE)
9028-17-5Q (XYLITOL DEHYDROGENASE)
9014-48-6 (TRANSKETOLASE)
9014-46-4 (TRANSALDOLASE)
58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)
64-17-5 (ETHANOL)
87-99-0 (XYLITOL)
50-99-7 (GLUCOSE)

L131 ANSWER 2 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1996:254078 BIOSIS
DN PREV199698810207
TI Process development of fuel **ethanol** production from lignocellulosic sugars using genetically engineered **yeasts**.
AU Krishnan, M. S. (1); Xia, Y.; **Ho, N. W. Y.**; Tsao, G. T. (1)
CS (1) Sch. Chem. Eng., Purdue Univ., West Lafayette, IN 47907 USA
SO Abstracts of Papers American Chemical Society, (1996) Vol. 211, No. 1-2, pp. BTEC 32.
Meeting Info.: 211th American Chemical Society National Meeting New Orleans, Louisiana, USA March 24-28, 1996
ISSN: 0065-7727.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Studies - General 10060
Biochemical Studies - Carbohydrates 10068
Biophysics - Bioengineering *10511
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation *51508
BC **Fungi - Unspecified *15000**
IT Major Concepts
Bioenergetics (Biochemistry and Molecular Biophysics); Bioprocess Engineering; General Life Studies; Genetics; Metabolism
IT Chemicals & Biochemicals
ETHANOL; GLUCOSE; XYLOSE
IT Miscellaneous Descriptors
FERMENTATION; **GLUCOSE**; MEETING ABSTRACT; **XYLOSE**
ORGN Super Taxa
Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungi (Fungi - Unspecified)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **64-17-5 (ETHANOL)**
50-99-7 (GLUCOSE)

58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)

L131 ANSWER 3 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:239232 BIOSIS
DN PREV199598253532
TI Saccharification and fermentation of dilute pretreated corn fiber to **ethanol** using a recombinant **xylose**-fermenting saccharomyces.
AU Xia, Youkun; **Ho, Nancy W. Y.**; Gong, C. S.; **Chen, Z. D.** ; Tsao, George T.
CS Lab. Renewable Resources Eng., Purdue Univ., West Lafayette, IN 47907-1295 USA
SO Abstracts of Papers American Chemical Society, (1995) Vol. 209, No. 1-2, pp. BIOT 72.
Meeting Info.: 209th American Chemical Society National Meeting Anaheim, California, USA April 2-6, 1995
ISSN: 0065-7727.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Biochemical Studies - General *10060
Biochemical Studies - Carbohydrates *10068
Biophysics - General Biophysical Techniques 10504
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents *51522
BC **Ascomycetes *15100**
IT Major Concepts
Biochemistry and Molecular Biophysics; Bioprocess Engineering
IT Chemicals & Biochemicals
ETHANOL; GLUCOSE; XYLOSE
IT Miscellaneous Descriptors
GLUCOSE; MEETING ABSTRACT; **XYLOSE**
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Ascomycetes (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **64-17-5 (ETHANOL)**
50-99-7 (GLUCOSE)
58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)

L131 ANSWER 4 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:50762 BIOSIS
DN PREV199598065062
TI Properties of the cyclase associated protein in **S. cerevisiae.**
AU Freeman, N.; Mintzer, K.; **Chen, Z.**; Weber, A.; Field, J.
CS Dep. Pharmacol., Univ. Pennsylvania Sch. Med., 36th and Hamilton Walk, Philadelphia, Pa 19104-6084 USA
SO Molecular Biology of the Cell, (1994) Vol. 5, No. SUPPL., pp. 12A.
Meeting Info.: Thirty-fourth Annual Meeting of the American Society for Cell Biology San Francisco, California, USA December 10-14, 1994
ISSN: 1059-1524.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520

Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biophysics - Molecular Properties and Macromolecules 10506
Biophysics - Membrane Phenomena *10508
Enzymes - Physiological Studies *10808
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
BC **Ascomycetes *15100**
IT Major Concepts
Enzymology (Biochemistry and Molecular Biophysics); Genetics; Membranes (Cell Biology)
IT Chemicals & Biochemicals
CYCLASE; CYCLIC AMP
IT Miscellaneous Descriptors
ACTIN BINDING PROTEIN; CYCLIC AMP; MEETING ABSTRACT; MEETING POSTER; MOLECULAR BIOLOGY
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Saccharomyces cerevisiae (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN 9074-90-2 (CYCLASE)
60-92-4 (CYCLIC AMP)

L131 ANSWER 5 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1994:418634 BIOSIS
DN PREV199497431634
TI Genetic improvement of **Saccharomyces cerevisiae** for **ethanol production** from **xylose**.
AU Tantirungkij, Manee; Seki, Tatsuji (1); Yoshida, Toshiomi
CS (1) Int. Cent. Cooperative Res. Biotechnol. Japan, Fac. Eng., Osaka Univ., Suita-shii, Osaka 565 Japan
SO Bajpai, R. K. [Editor]; Prokop, A. [Editor]. Annals of the New York Academy of Sciences, (1994) Vol. 721, pp. 138-147. Annals of the New York Academy of Sciences; Recombinant DNA technology II.
Publisher: New York Academy of Sciences 2 East 63rd Street, New York, New York 10021, USA.
Meeting Info.: Conference Palm Coast, Florida, USA January 31-February 5, 1993
ISSN: 0077-8923. ISBN: 0-89766-822-7 (paper), 0-89766-821-9 (cloth).
DT Book; Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Methods - General *10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Enzymes - Methods *10804
Enzymes - Physiological Studies 10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Microbiological Apparatus, Methods and Media *32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents 51522
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods

*51524
BC **Ascomycetes *15100**
IT Major Concepts
Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques
IT Chemicals & Biochemicals
ETHANOL; XYLOSE; XYLOSE REDUCTASE ; XYLITOL DEHYDROGENASE
IT Miscellaneous Descriptors
BIOTECHNOLOGY; BOOK CHAPTER; GENETIC ENGINEERING; MEETING PAPER; SYNTHETIC METHOD; **XYLITOL DEHYDROGENASE** GENE; **XYLOSE REDUCTASE** GENE
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **64-17-5 (ETHANOL)**
58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)
95829-40-6 (XYLOSE REDUCTASE)
9028-16-4Q (XYLITOL DEHYDROGENASE)
9028-17-5Q (XYLITOL DEHYDROGENASE)

L131 ANSWER 6 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1994:194149 BIOSIS
DN PREV199497207149
TI Fermentation of lignocellulose hydrolysates.
AU Hahn-Hagerdal, B.
CS Dep. Applied Microbiol., Lund Inst. Technol., Lund Univ., P.O. Box 124, S-221 OO Lund Sweden
SO Abstracts of Papers American Chemical Society, (1994) Vol. 207, No. 1-2, pp. BTEC 168.
Meeting Info.: 207th National Meeting of the American Chemical Society San Diego, California, USA March 13-17, 1994
ISSN: 0065-7727.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Methods - General *10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Carbohydrates *10058
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods *51524
BC **Ascomycetes *15100**
IT Major Concepts
Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques
IT Chemicals & Biochemicals
LIGNOCELLULOSE; **XYLOSE REDUCTASE; XYLITOL**

DEHYDROGENASE; XYLITOL; **ETHANOL**
IT Miscellaneous Descriptors
BIOTECHNOLOGY; **ETHANOL PRODUCTION**; GENETIC ENGINEERING; MEETING ABSTRACT; SYNTHETIC METHOD; **XYLITOL DEHYDROGENASE** GENE; XYLITOL PRODUCTION; **XYLOSE REDUCTASE** GENE
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN 11132-73-3 (LIGNOCELLULOSE)
95829-40-6 (XYLOSE REDUCTASE)
9028-16-4Q (XYLITOL DEHYDROGENASE)
9028-17-5Q (XYLITOL DEHYDROGENASE)
87-99-0 (XYLITOL)
64-17-5 (ETHANOL)

L131 ANSWER 7 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1993:424217 BIOSIS
DN PREV199345071842
TI Cloning and improving the expression of Pichia stipitis **xylose** reductase gene in **Saccharomyces cerevisiae.**
AU **Chen, Zhengdao; Ho, Nancy W. Y. (1)**
CS (1) Lab. Renewable Resources Eng., Purdue Univ., 1295 Potter Cent., West Lafayette, IN 47907-1295 USA
SO Applied Biochemistry and Biotechnology, (1993) Vol. 39-40, No. 0, pp. 135-147.
Meeting Info.: Fourteenth Symposium on Biotechnology for Fuels and Chemicals Gatlinburg, Tennessee, USA May 11-15, 1992
ISSN: 0273-2289.
DT Article
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General 10010
Biochemical Methods - General 10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - General *10060
Replication, Transcription, Translation *10300
Enzymes - General and Comparative Studies; Coenzymes 10802
Enzymes - Methods 10804
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Proteins, Peptides and Amino Acids 13012
Metabolism - Nucleic Acids, Purines and Pyrimidines 13014
Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents *51522
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
Plant Physiology, Biochemistry and Biophysics - General and Miscellaneous *51526

BC **Ascomycetes *15100**
IT Major Concepts
Biochemistry and Molecular Biophysics; Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics); Physiology
IT Chemicals & Biochemicals
XYLOSE REDUCTASE; **ALCOHOL** DEHYDROGENASE
IT Miscellaneous Descriptors
ALCOHOL DEHYDROGENASE; BIOMASS; BIOTECHNOLOGY; GENETIC ENGINEERING; PROMOTER; TRANSCRIPTION; TRANSLATION
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN 95829-40-6 (**XYLOSE** REDUCTASE)
9031-72-5 (**ALCOHOL** DEHYDROGENASE)

L131 ANSWER 8 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1992:247463** BIOSIS
DN **BR42:117763**
TI THE USE OF **GENETIC ENGINEERING METHODS** TO IMPROVE FERMENTATION PROCESSES.
AU BEN-BASSAT A
CS CETUS CORP., 1400 FIFTY-THIRD STREET, EMERYVILLE, CALIF. 94608.
SO WHITE, M. D., S. REUVENY AND A. SHAFFERMAN (ED.). BIOLOGICALS FROM RECOMBINANT MICROORGANISMS AND ANIMAL CELLS: PRODUCTION AND RECOVERY; 34TH OHOLO CONFERENCE, EILAT, ISRAEL, 1990. XV+567P. VCH VERLAGSGESELLSCHAFT MBH: WEINHEIM, GERMANY; VCH PUBLISHERS, INC.: NEW YORK, NEW YORK, USA; BALABAN PUBLISHERS: REHOVOT, ISRAEL. ILLUS. (1991) 0 (0), 17-31. ISBN: 3-527-28084-7 (CLOTH), 0-89573-967-4 (PAPER).
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General 03502
Genetics and Cytogenetics - Plant *03504
Biochemical Methods - General *10050
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Methods - Carbohydrates *10058
Replication, Transcription, Translation 10300
Enzymes - Methods *10804
Metabolism - General Metabolism; Metabolic Pathways 13002
Metabolism - Carbohydrates 13004
Metabolism - Proteins, Peptides and Amino Acids 13012
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Food and Industrial Microbiology - General and Miscellaneous *39008
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents 51522
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
BC Acetobacteraceae 06501
Enterobacteriaceae 06702

Ascomycetes 15100
Fungi Imperfecti or Deuteromycetes 15500
IT Miscellaneous Descriptors
ASPERGILLUS-AWAMORI GLUCOAMYLASE GENE CLONING **SACCHAROMYCES-CEREVISIAE** ESCHERICHIA-COLI GENE CLONING CORN STARCH TO **ETHANOL** METHIONINE AMINOPEPTIDASE GENE CLONING RECOMBINANT PROTEIN INITIATION METHIONINE RESIDUE REMOVAL LOW ACETATE PRODUCING MUTANT USE HIGHER RECOMBINANT PROTEIN **PRODUCTION** **GLUCOSE** DEHYDROGENASE NEGATIVE ACETOBACTER-XYLINUM MUTANT CELLULOSE **PRODUCTION** GENETICALLY ENGINEERED ORGANISM GENETICALLY ENGINEERED PRODUCT SYNTHETIC METHOD BIOTECHNOLOGY
RN 63-68-3 (METHIONINE)
64-17-5 (ETHANOL)
71-50-1 (ACETATE)
9004-34-6 (CELLULOSE)
9005-25-8 (CORN STARCH)
9032-08-0 (GLUCOAMYLASE)
61229-81-0 (METHIONINE AMINOPEPTIDASE)
9028-53-9Q, 37250-49-0Q, 37250-50-3Q, 37250-84-3Q (**GLUCOSE** DEHYDROGENASE)

L131 ANSWER 9 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1991:423012 BIOSIS
DN BR41:72557
TI GENETIC TRANSFORMATION OF **XYLOSE**-FERMENTING **YEAST** PICHIA-STIPITIS.
AU **HO N W Y**; PETROS D; DENG X X
CS LAB. RENEWABLE RES. ENG., PURDUE UNIVERSITY, WEST LAFAYETTE, INDIANA 47907.
SO TWELFTH SYMPOSIUM ON BIOTECHNOLOGY FOR FUELS AND CHEMICALS, GATLINBURG, TENNESSEE, USA, MAY 7-11, 1990. APPL BIOCHEM BIOTECHNOL. (1991) 28-29 (0), 369-376.
CODEN: ABIBDL. ISSN: 0273-2289.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Carbohydrates 10068
Replication, Transcription, Translation 10300
Biophysics - Bioengineering *10511
Metabolism - Carbohydrates *13004
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
BC **Ascomycetes 15100**
IT Miscellaneous Descriptors
SACCHAROMYCES-CEREVISIAE 2 MICRON REPLICON ELECTROPORATION

L131 ANSWER 10 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1991:330572 BIOSIS
DN BR41:27122
TI ENGINEERING OF **XYLOSE** METABOLIC PATHWAY IN **SACCHAROMYCES -CEREVISIAE**.
AU **HO N W Y**; DENG S X X; CHEN J D
CS LAB. RENEWABLE RESOURCES ENG., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907-1294.
SO 75TH ANNUAL MEETING OF THE FEDERATION OF AMERICAN SOCIETIES FOR EXPERIMENTAL BIOLOGY, ATLANTA, GEORGIA, USA, APRIL 21-25, 1991. FASEB (FED AM SOC EXP BIOL) J. (1991) 5 (6), A1510.
CODEN: FAJOEC. ISSN: 0892-6638.

DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Food and Industrial Microbiology - Food and Beverage Fermentation *39003
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
BC **Ascomycetes 15100**
IT Miscellaneous Descriptors
ABSTRACT PICHIA-STIPITIS **XYLOSE REDUCTASE** **XYLITOL DEHYDROGENASE XYLULOKINASE** PENTOSE PATHWAY **ALCOHOL** FERMENTATION GENETIC ENGINEERING
RN **64-17-5 (ALCOHOL)**
9030-58-4 (XYLULOKINASE)
53106-52-8 (PENTOSE)
95829-40-6 (XYLOSE REDUCTASE)
58-86-6Q, 25990-60-7Q (XYLOSE)
9028-16-4Q, 9028-17-5Q (XYLITOL DEHYDROGENASE)

L131 ANSWER 11 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1990:346956 BIOSIS
DN BR39:42217
TI RECOMBINANT RHIZOPUS PEPSINOGEN.
AU **CHEN Z**; HAN H-P; HARTSUCK J A; TANG J
CS OKLA. MED. RES. FOUND., UNIV. OKLA. HEALTH SCI. CENT., OKLAHOMA CITY, OKLA. 73104, USA.
SO JOINT MEETING OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY, AND THE AMERICAN ASSOCIATION OF IMMUNOLOGISTS, NEW ORLEANS, LOUISIANA, USA, JUNE 4-7, 1990. FASEB (FED AM SOC EXP BIOL) J. (1990) 4 (7), A2119.
CODEN: FAJOEC. ISSN: 0892-6638.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Cytology and Cytochemistry - Plant *02504
Genetics and Cytogenetics - Plant *03504
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biophysics - Molecular Properties and Macromolecules 10506
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Metabolism - Proteins, Peptides and Amino Acids *13012
Genetics of Bacteria and Viruses 31500
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
BC Enterobacteriaceae 04810
Phycomycetes 15900
IT Miscellaneous Descriptors
ABSTRACT RHIZOPUS-CHINENSIS ESCHERICHIA-COLI ZYMOGEN SECRETORY VESICAL ACTIVATION MOLECULAR SEQUENCE DATA AMINO ACID SEQUENCE

RN 9001-10-9 (PEPSINOGEN)

L131 ANSWER 12 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1990:345669 BIOSIS
DN BR39:40930
TI XYLULOKINASE ACTIVITY IN VARIOUS **YEASTS** INCLUDING **SACCHAROMYCES-CEREVISIAE** CONTAINING THE CLONED XYLULOKINASE GENE.
AU DENG X X; **HO N W Y**
CS DEP. FOOD NUTR., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907, USA.
SO ELEVENTH SYMPOSIUM ON BIOTECHNOLOGY FOR FUELS AND CHEMICALS, COLORADO SPRINGS, COLORADO, USA, MAY 8-12, 1989. APPL BIOCHEM BIOTECHNOL. (1990) 24-25 (SPRING-SUMMER), 193-200.
CODEN: ABIBDL. ISSN: 0273-2289.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Carbohydrates 10058
Biochemical Studies - Carbohydrates 10068
Enzymes - Methods *10804
Enzymes - Chemical and Physical 10806
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
Microbiological Apparatus, Methods and Media 32000
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
BC Enterobacteriaceae 04810
Ascomycetes 15100
IT Miscellaneous Descriptors
ESCHERICHIA-COLI GENETIC ENGINEERING BIOTECHNOLOGY
RN 9030-58-4 (XYLULOKINASE)

L131 ANSWER 13 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1990:300917 BIOSIS
DN BR39:19098
TI DEVELOPMENT OF A GENETIC TRANSFORMATION SYSTEM FOR **YEAST** PICHIA-STIPITIS.
AU **HO N W Y**; DENG X X
CS LABORATORY RENEWABLE RESOURCES ENGINEERING, A. A. POTTER ENGINEERING BUILDING, PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907.
SO 199TH ACS (AMERICAN CHEMICAL SOCIETY) NATIONAL MEETING, BOSTON, MASSACHUSETTS, USA, APRIL 22-27, 1990. ABSTR PAP AM CHEM SOC. (1990) 199 (1-2), BIOT 125.
CODEN: ACSRAL. ISSN: 0065-7727.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Replication, Transcription, Translation *10300
Biophysics - Bioengineering *10511
Metabolism - Carbohydrates *13004
Metabolism - Proteins, Peptides and Amino Acids *13012
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519

BC **Ascomycetes 15100**
IT Miscellaneous Descriptors
ABSTRACT RECOMBINANT DNA TECHNIQUE FOREIGN PROTEIN OVEREXPRESSION **GLUCOSE XYLOSE** METABOLISM
RN **50-99-7 (GLUCOSE)**
58-86-6Q, 25990-60-7Q (XYLOSE)

L131 ANSWER 14 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1989:526586 BIOSIS
DN BR37:125444
TI CONSTRUCTION OF **YEAST** XYLULOKINASE MUTANT BY RECOMBINANT DNA TECHNIQUES SCIENTIFIC NOTE.
AU STEVIS P E; **HO N W Y**
CS LAB. RENEW. RESOUR. ENG., DEP. FOODS NUTR., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907, USA.
SO TENTH SYMPOSIUM ON BIOTECHNOLOGY FOR FUELS AND CHEMICALS, GATLINBURG, TENNESSEE, USA, MAY 16-20, 1988. APPL BIOCHEM BIOTECHNOL. (1989) 20-21 (0), 327-334.
CODEN: ABIBDL. ISSN: 0273-2289.
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Cytology and Cytochemistry - Plant 02504
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General 10010
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Replication, Transcription, Translation 10300
Biophysics - Molecular Properties and Macromolecules 10506
Enzymes - Methods *10804
Enzymes - Chemical and Physical 10806
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Metabolism - Proteins, Peptides and Amino Acids 13012
Metabolism - Nucleic Acids, Purines and Pyrimidines 13014
Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - General and Miscellaneous *51526
BC **Ascomycetes 15100**
IT Miscellaneous Descriptors
SACCHAROMYCES-CEREVISIAE GENE CLONING ENZYME ACTIVITY GENETIC ENGINEERING BIOTECHNOLOGY
RN 9030-58-4 (XYLULOKINASE)

L131 ANSWER 15 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1988:497081 BIOSIS
DN BR35:115916
TI A NEW HOST-VECTOR SYSTEM FOR THE STUDY OF **YEAST XYLOSE** FERMENTATION.
AU STEVIS P E; DENG X X; **HO N W Y**
CS LAB. RENEWABLE RESOURCES ENG., POTTER CENT., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907.
SO 196TH AMERICAN CHEMICAL SOCIETY NATIONAL MEETING, LOS ANGELES, CALIFORNIA, USA, SEPTEMBER 25-30, 1988. ABSTR PAP AM CHEM SOC. (1988) 196 (0), MBTD 100.
CODEN: ACSRAL. ISSN: 0065-7727.
DT Conference

FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Biochemical Methods - General *10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Carbohydrates *10058
Enzymes - Methods *10804
Enzymes - Physiological Studies 10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Physiology and Biochemistry of Bacteria 31000
Genetics of Bacteria and Viruses *31500
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
BC Enterobacteriaceae 04810
Ascomycetes 15100
IT Miscellaneous Descriptors
ABSTRACT ESCHERICHIA-COLI **SACCHAROMYCES-CEREVISIAE** **ALCOHOL** PRODUCTION BIOTECHNOLOGY GENETIC ENGINEERING XYLOKINASE
RN **64-17-5 (ALCOHOL)**
58-86-6Q, 25990-60-7Q (XYLOSE)

L131 ANSWER 16 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1986:80041 BIOSIS
DN BR30:80041
TI GENETIC ENGINEERING OF **YEASTS** FOR IMPROVED **XYLOSE** FERMENTATION.
AU **HO N W Y**; TSAO G T
CS LAB. RENEWABLE RESOURCES ENG., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907.
SO 190TH AMERICAN CHEMICAL SOCIETY NATIONAL MEETING, CHICAGO, ILL., USA, SEPT. 8-13, 1985. ABSTR PAP AM CHEM SOC. (**1985 (RECD 1986)**) 190 (0), NO PAGINATION.
CODEN: ACSRAL. ISSN: 0065-7727.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General 10010
Biochemical Methods - General 10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates *10068
Replication, Transcription, Translation 10300
Biophysics - Molecular Properties and Macromolecules *10506
Enzymes - General and Comparative Studies; Coenzymes 10802
Enzymes - Methods *10804
Enzymes - Chemical and Physical 10806
Enzymes - Physiological Studies 10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Metabolism - Proteins, Peptides and Amino Acids 13012
Metabolism - Nucleic Acids, Purines and Pyrimidines 13014

Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
BC **Ascomycetes 15100**
Fungi Imperfecti or Deuteromycetes 15500
IT Miscellaneous Descriptors
ABSTRACT CLONING ENZYMES TRANSFORMATION SYSTEMS BIOTECHNOLOGY
RN **58-86-6Q, 25990-60-7Q (XYLOSE)**

L131 ANSWER 17 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1985:172903 BIOSIS
DN BR29:62899
TI DEVELOPMENT OF A CLONING SYSTEM FOR CANDIDA-SPP.
AU **HO N W Y**; GAO H C; HUANG J J; STEVIS P E; CHANG S F; TSAO G T
CS LAB. RENEWABLE RESOURCES ENG., PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907, USA.
SO SCOTT, C. D. (ED.). BIOTECHNOLOGY AND BIOENGINEERING SYMPOSIUM, NO. 14. SIXTH SYMPOSIUM ON BIOTECHNOLOGY FOR FUELS AND CHEMICALS; GATLINBURG, TENN., USA, MAY 15-18, 1984. VIII+697P. JOHN WILEY & SONS, INC.: NEW YORK, N.Y., USA. ILLUS. PAPER. (**1984 (RECD 1985)**) 0 (0), 295-302. CODEN: BIBSBR. ISSN: 0572-6565. ISBN: 0-471-81332-.
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General 10010
Biochemical Methods - General 10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Metabolism - General Metabolism; Metabolic Pathways 13002
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - General and Miscellaneous *39008
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents 51522
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
BC **Fungi Imperfecti or Deuteromycetes 15500**
IT Miscellaneous Descriptors
GENETIC MARKERS DNA REPLICATION INDUSTRIAL MICROORGANISMS BIOTECHNOLOGY

L131 ANSWER 18 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1985:54877 BIOSIS
DN BR28:54877
TI EXPRESSION OF THE ESCHERICHIA-COLI **XYLOSE** ISOMERASE EC-5.3.1.5 GENE BY A **YEAST SACCHAROMYCES-CEREVISIAE** PROMOTER.
AU **HO N W Y**; STEVIS P; ROSENFELD S; HUANG J J; TSAO G T
CS LAB. RENEWABLE RESOURCES ENGINEERING, PURDUE UNIV., WEST LAFAYETTE, INDIANA 47907.
SO SCOTT, C. D. (ED.). BIOTECHNOLOGY AND BIOENGINEERING SYMPOSIUM, NO. 13. 5TH SYMPOSIUM ON BIOTECHNOLOGY FOR FUELS AND CHEMICALS; GATLINBURG, TENN., USA, MAY 10-13, 1983. VIII+672P. JOHN WILEY AND SONS, INC.: NEW YORK, N.Y., USA. ILLUS. PAPER. (1984) 0 (0), 245-250.

CODEN: BIBSBR. ISSN: 0572-6565. ISBN: 0-471-88173-2.
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General 10010
Biochemical Methods - General 10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Replication, Transcription, Translation 10300
Biophysics - Molecular Properties and Macromolecules *10506
Biophysics - Bioengineering 10511
Enzymes - Methods *10804
Metabolism - General Metabolism; Metabolic Pathways 13002
Metabolism - Energy and Respiratory Metabolism 13003
Metabolism - Carbohydrates 13004
Metabolism - Proteins, Peptides and Amino Acids 13012
Metabolism - Nucleic Acids, Purines and Pyrimidines 13014
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
Microbiological Apparatus, Methods and Media 32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
BC Enterobacteriaceae 04810
Ascomycetes 15100
IT Miscellaneous Descriptors
GENETIC ENGINEERING BIOTECHNOLOGY
RN 9023-82-9 (**XYLOSE** ISOMERASE)
9023-82-9 (EC-5.3.1.5)

L131 ANSWER 19 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1984:30947 BIOSIS
DN BR26:30947
TI CLONING OF THE ESCHERICHIA-COLI **XYLOSE** ISOMERASE GENE IN **YEAST SACCHAROMYCES-CEREVISIAE.**
AU **HO N W Y**; ROSENFELD S; STEVIS P
CS LAB. OF RENEWABLE RESOURCES ENGINEERING, PURDUE UNIV., WEST LAFAYETTE, IN 47907.
SO 74TH ANNUAL MEETING OF THE AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, SAN FRANCISCO, CALIF., USA, JUNE 5-9, 1983. FED PROC. (1983) 42 (7), ABSTRACT 2394.
CODEN: FEPRA7. ISSN: 0014-9446.
DT Conference
FS BR; OLD
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Plant *03504
Genetics and Cytogenetics - Animal *03506
Biochemical Methods - Proteins, Peptides and Amino Acids 10054
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Enzymes - Methods *10804
Enzymes - Physiological Studies *10808
BC Enterobacteriaceae 04810
Ascomycetes 15100
IT Miscellaneous Descriptors

ABSTRACT RESTRICTION ENDO NUCLEASE GENETIC ENGINEERING PROMOTER
RN 9023-82-9 (**XYLOSE** ISOMERASE)
9055-11-2 (ENDO NUCLEASE)

L131 ANSWER 20 OF 20 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1970:63316 BIOSIS
DN BR06:63316
TI A NEW CLEAVAGE METHOD FOR THE STUDY OF NUCLEOTIDE SEQUENCES IN RNA.
AU **HO N W Y**; UCHIDA T; EGAMI F; GILHAM P T
SO FRISCH, LEONORA (EDITED BY). COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY. VOL. XXXIV. THE MECHANISM OF PROTEIN SYNTHESIS. XXIV + 855P. ILLUS. COLD SPRING HARBOR LABORATORY: COLD SPRING HARBOR, L. I., N.Y., U.S.A. (1970) 647-650.
FS BR; OLD
LA Unavailable
CC **Genetics and Cytogenetics - Plant *03504**
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biophysics - Molecular Properties and Macromolecules *10506
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
BC **Fungi - Unspecified 15000**
IT Miscellaneous Descriptors
YEAST

=> d all tot 1133

L133 ANSWER 1 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1997:452608** BIOSIS
DN **PREV199799751811**
TI Expression of different levels of enzymes from the Pichia stipitis XYL1 and XYL2 genes in **Saccharomyces cerevisiae** and its effects on product formation during **xylose** utilisation.
AU Walfridsson, M.; Anderlund, M.; Bao, X.; Hahn-Hagerdal, B. (1)
CS (1) Dep. Appl. Microbiol., Lund Inst. Technol./Lund Univ., P.O. Box 124, S-221 00 Lund Sweden
SO Applied Microbiology and Biotechnology, (1997) Vol. 48, No. 2, pp. 218-224.
ISSN: 0175-7598.
DT Article
LA English
AB **Saccharomyces cerevisiae** was transformed with the Pichia stipitis CBS 6054 XYL1 and XYL2 genes encoding **xylose reductase** (XR) and **xylitol dehydrogenase** (XDH) respectively. The XYL1 and XYL2 genes were placed under the control of the alcohol dehydrogenase 1 (ADH1) and phosphoglycerate kinase (PGK1) promoters in the **yeast** vector YEp24. Different vector constructions were made resulting in different specific activities of XR and XDH. The XR:XDH ratio (ratio of specific enzyme activities) of the transformed **S. cerevisiae** strains varied from 17.5 to 0.06. In order to enhance **xylose** utilization in the XYL1-, XYL2-containing **S. cerevisiae** strains, the native genes encoding transketolase and transaldolase were also overexpressed. A strain with an XR:XDH ratio of 17.5 formed 0.82 g xylitol/g consumed **xylose**, whereas a strain with an XR:XDH ratio of 5.0 formed 0.58 g xylitol/g **xylose**. The strain with an XR:XDH ratio of 0.06, on the other hand, formed no xylitol and less glycerol and acetic acid compared with strains with the higher XR:XDH ratios. In addition, the strain with an XR:XDH ratio of 0.06 produced more **ethanol** than the other strains.
CC Clinical Biochemistry; General Methods and Applications *10006
Comparative Biochemistry, General *10010
Biochemical Methods - General *10050

Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Enzymes - General and Comparative Studies; Coenzymes *10802
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Nutrition - Carbohydrates *13220
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Nutrition *51504
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation *51508
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519

BC **Ascomycetes *15100**

IT Major Concepts
Biochemistry and Molecular Biophysics; Bioenergetics (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Clinical Chemistry (Allied Medical Sciences); Enzymology (Biochemistry and Molecular Biophysics); Metabolism; Methods and Techniques; Nutrition

IT Chemicals & Biochemicals
XYLOSE; XYLOSE REDUCTASE; XYLITOL DEHYDROGENASE; ALCOHOL DEHYDROGENASE; XYLITOL; GLYCEROL; ACETIC ACID; **ETHANOL**

IT Miscellaneous Descriptors
ACETIC ACID; ALCOHOL DEHYDROGENASE I; BIOBUSINESS; BIOPROCESS ENGINEERING; BIOTECHNOLOGY; ENZYME LEVELS; ENZYMES; ENZYMOLOGY; **ETHANOL; ETHANOL PRODUCTION**; GENE EXPRESSION; GENE OVEREXPRESSION; GLYCEROL; MOLECULAR GENETICS; PRODUCT FORMATION; PROMOTERS; TRANSFORMATION; XYLITOL; **XYLITOL DEHYDROGENASE; XYLOSE; XYLOSE REDUCTASE; XYLOSE** UTILIZATION; XYL1 GENE; XYL2 GENE; **YEAST** VECTOR

ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae

ORGN Organism Name
fungus (Fungi - Unspecified); **Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)**

ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants

RN **58-86-6Q (XYLOSE)**
25990-60-7Q (XYLOSE)
95829-40-6Q (XYLOSE REDUCTASE)
99775-25-4Q (XYLOSE REDUCTASE)
104118-53-8Q (XYLOSE REDUCTASE)
9028-16-4Q (XYLITOL DEHYDROGENASE)
9028-17-5Q (XYLITOL DEHYDROGENASE)
9031-72-5 (ALCOHOL DEHYDROGENASE)
87-99-0 (XYLITOL)
56-81-5 (GLYCEROL)
64-19-7 (ACETIC ACID)
64-17-5 (ETHANOL)

L133 ANSWER 2 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1997:318934** BIOSIS
DN **PREV199799609422**
TI Fermentation of corn fibre sugars by an engineered **xylose** utilizing Saccharomyces **yeast** strain.
AU Moniruzzaman, M.; Dien, B. S.; Skory, C. D.; **Chen, Z. D.**;

Hespell, R. B.; **Ho, N. W. Y.**; Dale, B. E.; Bothast, R. J. (1)
CS (1) Fermentation Biochem. Res. Unit, Natl. Cent. Agric. Utilization Res., USDA, Peoria, IL 61604 USA
SO World Journal of Microbiology & Biotechnology, (1997) Vol. 13, No. 3, pp. 341-346.
ISSN: 0959-3993.
DT Article
LA English
AB The ability of a recombinant Saccharomyces **yeast** strain to ferment the sugars **glucose**, **xylose**, arabinose and galactose which are the predominant monosaccharides found in corn fibre hydrolysates has been examined. Saccharomyces strain 1400 (pLNH32) was genetically engineered to ferment **xylose** by expressing genes encoding a **xylose** reductase, a xylitol dehydrogenase and a xylulose kinase. The recombinant efficiently fermented **xylose** alone or in the presence of **glucose**. **Xylose**-grown cultures had very little difference in xylitol accumulation, with only 4 to 5 g/l accumulating, in aerobic, micro-aerated and anaerobic conditions. Highest production of **ethanol** with all sugars was achieved under anaerobic conditions. From a mixture of **glucose** (80 g/l) and **xylose** (40 g/l), this strain produced 52 g/l **ethanol**, equivalent to 85% of theoretical yield, in less than 24 h. Using a mixture of **glucose** (31 g/l), **xylose** (15.2 g/l), arabinose (10.5 g/l) and galactose (2 g/l), all of the sugars except arabinose were consumed in 24 h with an accumulation of 22 g **ethanol**/l, a 90% yield (excluding the arabinose in the calculation since it is not fermented). Approximately 98% theoretical yield, or 21 g **ethanol** /l, was achieved using an enzymatic hydrolysate of ammonia fibre exploded corn fibre containing an estimated 47.0 g mixed sugars/l. In all mixed sugar fermentations, less than 25% arabinose was consumed and converted into arabitol.
CC **Genetics and Cytogenetics - Plant *03504**
Enzymes - Physiological Studies *10808
Metabolism - Carbohydrates *13004
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
BC **Ascomycetes *15100**
IT Major Concepts
Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism
IT Chemicals & Biochemicals
XYLOSE; **XYLOSE** REDUCTASE; XYLITOL DEHYDROGENASE; KINASE; ARABITOL; **ETHANOL**; **GLUCOSE**; ARABINOSE; GALACTOSE
IT Industry
biotechnology industry
IT Miscellaneous Descriptors
ARABINOSE; ARABITOL; BIOBUSINESS; BIOPROCESS ENGINEERING; CELLULOSIC BIOMASS CONVERSION; CORN FIBER SUGARS; ENZYMOLOGY; **ETHANOL**; FERMENTATION; GALACTOSE; GENETICALLY ENGINEERED ORGANISM; **GLUCOSE**; MIXED SUGAR FERMENTATION; MOLECULAR GENETICS; PRODUCTION; STRAIN-1400; XYLITOL DEHYDROGENASE; **XYLOSE**; **XYLOSE** REDUCTASE; XYLULOSE KINASE
ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungus (Fungi - Unspecified); **Saccharomyces sp. (Ascomycetes)**
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **58-86-6Q (XYLOSE)**

25990-60-7Q (XYLOSE)
95829-40-6Q (**XYLOSE** REDUCTASE)
99775-25-4Q (**XYLOSE** REDUCTASE)
104118-53-8Q (**XYLOSE** REDUCTASE)
9028-16-4Q (XYLITOL DEHYDROGENASE)
9028-17-5Q (XYLITOL DEHYDROGENASE)
9031-44-1 (KINASE)
2152-56-9 (ARABITOL)
64-17-5 (ETHANOL)
50-99-7 (GLUCOSE)
147-81-9 (ARABINOSE)
59-23-4Q (GALACTOSE)
26566-61-0Q (GALACTOSE)
50855-33-9Q (GALACTOSE)

L133 ANSWER 3 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1997:294650** BIOSIS
DN **PREV199799593853**
TI Enhanced cofermentation of **glucose** and **xylose** by recombinant Saccharomyces **yeast** strains in batch and continuous operating modes.
AU Toon, Susan T.; Philippidis, George P.; **Ho, Nancy W. Y.**; **Chen, Zhengdao**; Brainard, Adam; Lumpkin, Robert E.; Riley, Cynthia J. (1)
CS (1) Biotechnology Cent. Fuels Chemicals, National Renewable Energy Lab., 1617 Cole Boulevard, Golden, CO 80401 USA
SO Applied Biochemistry and Biotechnology, (1997) Vol. 63-65, No. 0, pp. 243-255.
ISSN: 0273-2289.
DT Article
LA English
AB Agricultural residues, such as grain by-products, are rich in the hydrolyzable carbohydrate polymers hemicellulose and cellulose; hence, they represent a readily available source of the fermentable sugars **xylose** and **glucose**. The biomass-to-**ethanol** technology is now a step closer to commercialization because a stable recombinant **yeast** strain has been developed that can efficiently ferment **glucose** and **xylose** simultaneously (coferment) to **ethanol**. This strain, LNH-ST, is a derivative of Saccharomyces **yeast** strain 1400 that carries the **xylose** -catabolism encoding genes of Pichia stipitis in its chromosome. Continuous pure sugar cofermentation studies with this organism resulted in promising steady-state **ethanol** yields (70.4% of theoretical based on available sugars) at a residence time of 48 h. Further studies with corn biomass pretreated at the pilot scale confirmed the performance characteristics of the organism in a simultaneous saccharification and cofermentation (SSCF) process: LNH-ST converted 78.4% of the available **glucose** and 56.1% of the available **xylose** within 4 d, despite the presence of high levels of metabolic inhibitors. These SSCF data were reproducible at the bench scale and verified in a 9000-L pilot scale bioreactor.
CC **Genetics and Cytogenetics - Plant *03504**
Comparative Biochemistry, General *10010
Biochemical Studies - General *10060
Biochemical Studies - Carbohydrates *10068
Biophysics - Bioengineering *10511
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Microbiological Apparatus, Methods and Media *32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation

*51508
Plant Physiology, Biochemistry and Biophysics - Growth, Differentiation
*51510
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods
*51524
BC **Ascomycetes *15100**
IT Major Concepts
Biochemistry and Molecular Biophysics; Bioenergetics (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Development; General Life Studies; Genetics; Metabolism; Methods and Techniques
IT Chemicals & Biochemicals
GLUCOSE; XYLOSE; CELLULOSE; HEMICELLULOSE; **ETHANOL**
IT Miscellaneous Descriptors
BATCH CULTURE; BIOBUSINESS; BIOPROCESS ENGINEERING; BIOREACTOR; BIOTECHNOLOGY; CELLULOSE; CHROMOSOME; CONTINUOUS CULTURE; CULTURE METHOD; **ETHANOL; GLUCOSE**; HEMICELLULOSE; INDUSTRIAL EQUIPMENT; INDUSTRIAL **ETHANOL** PRODUCTION; METABOLISM; RECOMBINANT **YEASTS**; SACCHARIFICATION; STRAIN-LNH-ST; STRAIN-1400; SUGAR COFERMENTATIONS; SUGARS; **XYLOSE**
ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungus (Fungi - Unspecified); **Pichia stipitis (Ascomycetes)**; **Saccharomyces sp. (Ascomycetes)**
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **50-99-7 (GLUCOSE)**
58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)
9004-34-6 (CELLULOSE)
9034-32-6 (HEMICELLULOSE)
64-17-5 (ETHANOL)

L133 ANSWER 4 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1996:507311** BIOSIS
DN **PREV199699229667**
TI **Ethanol** production from corn cob pretreated by the ammonia steeping process using genetically engineered **yeast**.
AU Cao, N. J. (1); Krishnan, M. S.; Du, J. X.; Gong, C. S.; **Ho, N. W. Y.**; **Chen, Z. D.**; Tsao, G. T.
CS (1) Lab. Renewable Resources Eng., Purdue Univ., West Lafayette, IN 47907 USA
SO Biotechnology Letters, (1996) Vol. 18, No. 9, pp. 1013-1018.
ISSN: 0141-5492.
DT Article
LA English
AB A new and effective pretreatment process for biomass conversion involves the steeping of biomass in 2.9 M NH-4OH. This resulted in the removing about 80-90% of the lignin along with almost all the acetate from cellulosic residues. Based on dry cellulose from corn cob, a high **glucose** yield of 92% was obtained after enzymatic saccharification of cellulose fraction. By using a genetically engineered, xylosefermenting Saccharomyces 1400(pLNH33) in the batch fermentation of a **glucose -xylose** mixture from corn cob, an **ethanol** concentration of 47 g/L was obtained within 36 h with 84% yield. In addition, an **ethanol** concentration of 45 g/L was obtained within 48 h with 86% yield using simultaneous saccharification-fermentation process.
CC **Genetics and Cytogenetics - General *03502**
Genetics and Cytogenetics - Plant *03504

Comparative Biochemistry, General *10010
Biochemical Methods - General *10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - General *10060
Biochemical Studies - Carbohydrates *10068
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Microbiological Apparatus, Methods and Media *32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Nutrition *51504
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents *51522

BC **Ascomycetes *15100**

IT Major Concepts
Biochemistry and Molecular Biophysics; Bioprocess Engineering; Genetics; Metabolism; Methods and Techniques; Nutrition

IT Chemicals & Biochemicals
ETHANOL; AMMONIA

IT Miscellaneous Descriptors
BIOMASS CONVERSION; BIOPROCESS ENGINEERING; BIOTECHNOLOGY; CORN COB PRETREATED BY AMMONIA STEEPING PROCESS; **ETHANOL** PRODUCTION; FERMENTATION; GENETIC ENGINEERING; MISCELLANEOUS METHOD; SACCHARIFICATION

ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae

ORGN Organism Name
fungus (Fungi - Unspecified); **yeast** (Fungi - Unspecified); **Saccharomyces cerevisiae (Ascomycetes)**

ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants

RN **64-17-5 (ETHANOL)**
7664-41-7 (AMMONIA)

L133 ANSWER 5 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AN **1996:130023** BIOSIS

DN **PREV199698702158**

TI A heterologous reductase affects the redox balance of recombinant **Saccharomyces cerevisiae**.

AU Meinander, Nina; Zacchi, Guido; Hahn-Hagerdal, Barbel (1)

CS (1) Applied Microbiol., Lund Inst. Technol., Univ. Lund, PO Box 124, S-22100 Lund Sweden

SO Microbiology (Reading), (1996) Vol. 142, No. 1, pp. 165-172.
ISSN: 1350-0872.

DT Article

LA English

AB Recombinant **Saccharomyces cerevisiae** harbouring the **xylose reductase** (XR) gene XYL1 from Pichia stipitis was grown in anoxic chemostat culture at two different dilution rates. At each dilution rate a transient experiment, encompassing a shift in the sugar content of the medium from **glucose** to **glucose** plus **xylose** was performed. The steady states at the beginning and the end of the transients were compared in terms of specific product fluxes from **glucose** metabolism. At both dilution rates, the specific glycerol flux decreased and the specific acetate and CO-2 fluxes increased. The specific **ethanol** flux was not affected. At the lower dilution rate, the production of biomass decreased during the transient, but at the higher dilution rate it increased. The changes in product pattern can be explained as being due to the redox perturbation caused by the consumption of reduced cofactors in the XR-catalysed

reaction. Regeneration of NAD partly through **xylose** reduction instead of glycerol production decreased the formation of glycerol. Additionally, **xylose** reduction activated those pathways which produce reduced cofactors, such as acetate formation and the pentose phosphate pathway, indicated by increased acetate and CO, production. The dual cofactor specificity of XR, with a preference for NADPH over NADH, was evident from the effects of **xylose** reduction on product fluxes. Comparison of the **xylose** reduction rates at low and high **glucose** flux indicated that the supply of reduced cofactors partly controlled the reaction rate. At the higher dilution rate, control by some other factor such as **xylose** transport or XR activity increased. Calculation of carbon balances at the steady states showed that all substrate carbon was recovered in biomass or products. Based on the specific product fluxes, calculations of quantitative cofactor balances at the steady states was attempted. However, sensitivity calculations showed that analysis errors in the range of 5% caused substantial errors in the cofactor balance, without affecting the carbon balance.

CC **Genetics and Cytogenetics - Plant *03504**
Biochemistry - Gases *10012
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Carbohydrates 10068
Biophysics - Bioenergetics: Electron Transport and Oxidative Phosphorylation *10510
Biophysics - Bioengineering *10511
Enzymes - General and Comparative Studies; Coenzymes *10802
Enzymes - Physiological Studies *10808
Metabolism - Energy and Respiratory Metabolism *13003
Microbiological Apparatus, Methods and Media *32000
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation *51508
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents *51522

BC **Ascomycetes *15100**

IT Major Concepts
Biochemistry and Molecular Biophysics; Bioenergetics (Biochemistry and Molecular Biophysics); Enzymology (Biochemistry and Molecular Biophysics); General Life Studies; Genetics; Metabolism; Methods and Techniques

IT Chemicals & Biochemicals
REDUCTASE; NAD; NADH; **XYLOSE REDUCTASE**

IT Miscellaneous Descriptors
ANOXIC CHEMOSTAT CULTURE; GENETIC ENGINEERING; NAD; NADH; **XYLOSE REDUCTASE** GENE XYL1

ORGN Super Taxa
Ascomycetes: Fungi, Plantae

ORGN Organism Name
Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)

ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants

RN 9037-80-3 (REDUCTASE)
53-84-9 (NAD)
58-68-4 (NADH)
95829-40-6Q (XYLOSE REDUCTASE)
99775-25-4Q (XYLOSE REDUCTASE)
104118-53-8Q (XYLOSE REDUCTASE)

L133 ANSWER 6 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1996:34665** BIOSIS
DN **PREV199698606800**

TI **Xylose**-metabolizing **Saccharomyces cerevisiae** strains overexpressing the TDKL1 and TAL1 genes encoding the pentose phosphate pathway enzymes transketolase and transaldolase.

AU Walfridsson, Mats; Hallborn, Johan; Penttila, Merja; Keranen, Sirkka; Hahn-Hagerdal, Barbel (1)
CS (1) Dep. Applied Microbiol., Lund Univ., PO Box 124, S-221 00 Lund Sweden

SO Applied and Environmental Microbiology, (1995) Vol. 61, No. 12, pp. 4184-4190.
ISSN: 0099-2240.
DT Article
LA English

AB **Saccharomyces cerevisiae** was metabolically engineered for **xylose** utilization. The Pichia stipitis CBS 6054 genes XYL1 and XYL2 encoding **xylose reductase** and **xylitol dehydrogenase** were cloned into **S. cerevisiae**. The gene products catalyze the two initial steps in **xylose** utilization which **S. cerevisiae** lacks. In order to increase the flux through the pentose phosphate pathway, the **S. cerevisiae** TKL1 and TAL1 genes encoding transketolase and transaldolase were overexpressed. A XYL1- and XYL2-containing **S. cerevisiae** strain overexpressing TAL1 (S104-TAL) showed considerably enhanced growth on **xylose** compared with a strain containing only XYL1 and XYL2. Overexpression of only TKL1 did not influence growth. The results indicate that the transaldolase level in **S. cerevisiae** is insufficient for the efficient utilization of pentose phosphate pathway metabolites. Mixtures of **xylose** and **glucose** were simultaneously consumed with the recombinant strain S104:TAL. The rate of **xylose** consumption was higher in the presence of **glucose**. **Xylose** was used for growth and xylitol formation, but not for **ethanol production**. Decreased oxygenation resulted in impaired growth and increased xylitol formation. Fermentation with strain S103-TAL, having a **xylose reductase/xylitol dehydrogenase** ratio of 0.5:30 compared with 4.2:5.8 for S104-TAL, did not prevent xylitol formation.

CC **Genetics and Cytogenetics - Plant *03504**
Biochemistry - Gases *10012
Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Carbohydrates 10068
Replication, Transcription, Translation *10300
Biophysics - Bioengineering *10511
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
Nutrition - Carbohydrates *13220
Food and Industrial Microbiology - Food and Beverage Fermentation *39003
Plant Physiology, Biochemistry and Biophysics - Nutrition *51504
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519

BC **Ascomycetes *15100**

IT Major Concepts
Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Foods; General Life Studies; Genetics; Metabolism; Molecular Genetics (Biochemistry and Molecular Biophysics); Nutrition

IT Chemicals & Biochemicals
XYLOSE; TRANSKETOLASE; TRANSALDOLASE; XYLITOL; **ETHANOL**

IT Miscellaneous Descriptors
DECREASED OXYGENATION; **ETHANOL PRODUCTION**;

FERMENTATION; GENETICALLY ENGINEERED ORGANISM; GROWTH ENHANCEMENT; XYLITOL FORMATION; **XYLOSE** UTILIZATION
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **58-86-6Q (XYLOSE)**
25990-60-7Q (XYLOSE)
9014-48-6 (TRANSKETOLASE)
9014-46-4 (TRANSALDOLASE)
87-99-0 (XYLITOL)
64-17-5 (ETHANOL)

L133 ANSWER 7 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1995:76968** BIOSIS
DN **PREV199598091268**
TI Fed-batch xylitol production with recombinant XYL-1-expressing **Saccharomyces cerevisiae** using **ethanol** as a co-substrate.
AU Meinander, N.; Hahn-Hagerdal, B.; Linko, M.; Linko, P.; Ojamo, H. (1)
CS (1) VTT, Biotechnical Lab., P.O. Box 202, SF-02151 Espoo Finland
SO Applied Microbiology and Biotechnology, (1994) Vol. 42, No. 2-3, pp. 334-339.
ISSN: 0175-7598.
DT Article
LA English
AB The bioconversion of **xylose** into xylitol in fed-batch fermentation with a recombinant **Saccharomyces cerevisiae** strain, transformed with the **xylose-reductase** gene of Pichia stipitis, was studied. When only **xylose** was fed into the fermentor, the production of xylitol continued until the **ethanol** that had been produced during an initial growth phase on **glucose** , was depleted. It was concluded that **ethanol** acted as a redox-balance-retaining co-substrate. The conversion of high amounts of **xylose** into xylitol required the addition of **ethanol** to the feed solution. Under O-2-limited conditions, acetic acid accumulated in the fermentation broth, causing poisoning of the **yeast** at low extracellular pH. Acetic acid toxicity could be avoided by either increasing the pH from 4.5 to 6.5 or by more effective aeration, leading to the further metabolism of acetic acid into cell mass. The best xylitol/**ethanol** yield, 2.4 g g-1 was achieved under O-2-limited conditions. Under anaerobic conditions **ethanol** could not be used as a co-substrate, because the cell cannot produce ATP for maintenance requirements from **ethanol** anaerobically. The specific rate of xylitol production decreased with increasing aeration. The initial volumetric productivity increased when **xylose** was added in portions rather than by continuous feeding, due to a more complete saturation of the transport system and the **xylose reductase** enzyme.
CC Cytology and Cytochemistry - Plant *02504
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General *10010
Biochemistry - Gases *10012
Biochemical Methods - General *10050
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Carbohydrates *10068
Biophysics - General Biophysical Studies *10502

Biophysics - Bioengineering *10511
Enzymes - Methods *10804
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Movement *12100
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
Nutrition - Carbohydrates *13220
Toxicology - General; Methods and Experimental *22501
Microbiological Apparatus, Methods and Media *32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Nutrition *51504
Plant Physiology, Biochemistry and Biophysics - Growth, Differentiation *51510
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods *51524
BC **Ascomycetes *15100**
IT Major Concepts
Biochemistry and Molecular Biophysics; Bioprocess Engineering; Cell Biology; Development; Enzymology (Biochemistry and Molecular Biophysics); General Life Studies; Genetics; Metabolism; Methods and Techniques; Nutrition; Physiology; Toxicology
IT Chemicals & Biochemicals
XYLITOL; **ETHANOL**; **XYLOSE**; OXYGEN
IT Miscellaneous Descriptors
BIOTECHNOLOGY; CELL MASS; ENZYMES; FERMENTATION; GENETIC ENGINEERING; GENETICS; METHODS; OXYGEN LIMITATION; PH; SPECIFIC PRODUCTION RATE; SUBSTRATES; SUGAR; TRANSFORMANTS; TRANSPORT SYSTEMS; **XYLOSE**
ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungus (Fungi - Unspecified); **Pichia stipitis (Ascomycetes)**; **Saccharomyces cerevisiae (Ascomycetes)**
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN 87-99-0 (XYLITOL)
64-17-5 (ETHANOL)
58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)
7782-44-7 (OXYGEN)

L133 ANSWER 8 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1994:531024** BIOSIS
DN **PREV199497544024**
TI Biochemistry and physiology of **xylose** fermentation by **yeasts**.
AU Hahn-Hagerdal, B. (1); Jeppsson, H.; Skoog, K.; Prior, B. A.
CS (1) Dep. Applied Microbiol., Chem. Cent., Lund Inst. Technol., Lund Univ., P.O. Box 124, S-221 00 Lund Sweden .
SO Enzyme and Microbial Technology, (1994) Vol. 16, No. 11, pp. 933-943. ISSN: 0141-0229.
DT General Review
LA English
AB The rate of **ethanol production** and the **ethanol** concentrations attained by the most promising **xylose**-fermenting **yeasts**, Pichia stipitis, Candida shehatae, and Pachysolen tannophilus, compare poorly with that of commercial **ethanol**

fermentation by non-**xylose**-fermenting **Saccharomyces cerevisiae** using **glucose**-based substrates. The oxygen requirement for efficient fermentation by the **xylose**-fermenting **yeasts** and the lack of such a general requirement by **S. cerevisiae** indicates basic underlying differences in their physiological relations to oxygen. The redox imbalance in the initial conversion of **xylose** to xylulose, sensitivity to high concentrations of **ethanol**, differences in the respiratory pathway and sensitivity to microbial inhibitors, particularly those liberated during pretreatment and hydrolysis of lignocellulose substrates, have been identified as major factors limiting **ethanol** fermentation by the **xylose**-fermenting **yeasts**. Recombinant **S. cerevisiae**, containing functional **xylose reductase** and **xylitol dehydrogenase**, grows on, but poorly ferments, **xylose**. The unfavorable kinetic properties of these enzymes and an inadequate pentose phosphate pathway apparently limit the ability of the recombinant **yeast** to ferment **xylose**.

CC Cytology and Cytochemistry - Plant *02504
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General *10010
Biochemistry - Gases *10012
Biochemical Methods - General *10050
Biochemical Studies - General *10060
Biochemical Studies - Carbohydrates *10068
Enzymes - General and Comparative Studies; Coenzymes *10802
Enzymes - Methods *10804
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Microbiological Apparatus, Methods and Media *32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation *51508
Plant Physiology, Biochemistry and Biophysics - Growth, Differentiation *51510
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents *51522
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods *51524

BC **Fungi - Unspecified *15000**

IT Major Concepts
Biochemistry and Molecular Biophysics; Bioenergetics (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Cell Biology; Development; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques

IT Chemicals & Biochemicals
XYLOSE; ALCOHOL; **ETHANOL**; OXYGEN

IT Miscellaneous Descriptors
ALCOHOL PRODUCTION; BIOTECHNOLOGY; ENZYME KINETIC PROPERTIES; **ETHANOL** CONCENTRATIONS; **ETHANOL PRODUCTION**; FERMENTATION; GENETIC ENGINEERING; METHODS; OXYGEN EFFECTS; RECOMBINANTS

ORGN Super Taxa
Fungi - Unspecified: Fungi, Plantae

ORGN Organism Name
fungi (Fungi - Unspecified); fungus (Fungi - Unspecified)

ORGN Organism Superterms

fungi; microorganisms; nonvascular plants; plants
RN **58-86-6Q (XYLOSE)**
25990-60-7Q (XYLOSE)
64-17-5 (ALCOHOL)
64-17-5 (ETHANOL)
7782-44-7 (OXYGEN)

L133 ANSWER 9 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1994:531023** BIOSIS
DN **PREV199497544023**
TI Strain selection, taxonomy, and genetics of **xylose**-fermenting **yeasts**.
AU Jeffries, T. W. (1); Kurtzman, C. P.
CS (1) Forest Prod. Lab., U.S. Dep. Agric., Forest Serv., Madison, WI 53705 USA
SO Enzyme and Microbial Technology, (1994) Vol. 16, No. 11, pp. 922-932. ISSN: 0141-0229.
DT General Review
LA English
AB **Xylose** utilization is essential for the efficient conversion of lignocellulose to **ethanol**. The objective of this review is to trace the development of **xylose**-fermenting **yeast** strains from their discovery in 1980. Following initial reports, screens of known **yeasts** identified five species of interest: Candida shehatae, Candida tenuis, Pachysolen tannophilus, Pichia segobiensis, and Pichia stipitis. Candida shehatae strains can be divided into three varieties. Pachysolen tannophilus and Pichia stipitis have been studied most extensively and have the best-understood genetic systems. Improved mutants of P. tannophilis have been obtained by selecting for an inability to oxidize **ethanol** (eth) and for rapid growth on xylitol and nitrate. Improved P. stipitis mutants have been obtained by selecting for flocculation, decreased utilization of **glucose**, and growth on noninductive carbon sources. Bacterial **xylose** isomerase has been cloned and expressed in **S. cerevisiae** and Schizosaccharomyces pombe, but the heterologous enzyme is inactive. **Xylose reductase** and **xylitol dehydrogenase** have been cloned from P. stipitis and expressed in **Saccharomyces cerevisiae**, giving rise to transformant **S. cerevisiae** that grow on **xylose** but that ferment it poorly. A transformation and expression system based on the URA3 marker has recently been developed for P. stipitis so that contemporary genetic methods may be brought to bear on this organism.
CC General Biology - Taxonomy, Nomenclature and Terminology *00504
General Biology - Conservation, Resource Management *00512
Cytology and Cytochemistry - Plant *02504
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General *10010
Biochemical Methods - General *10050
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - General *10060
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Carbohydrates *10068
Biophysics - Molecular Properties and Macromolecules *10506
Enzymes - General and Comparative Studies; Coenzymes *10802
Enzymes - Methods *10804
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Nutrition - Carbohydrates *13220
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007

Botany, General and Systematic - Fungi *50506
Plant Physiology, Biochemistry and Biophysics - Nutrition *51504
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation *51508
Plant Physiology, Biochemistry and Biophysics - Growth, Differentiation *51510
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
BC **Fungi - Unspecified *15000**
IT Major Concepts
Biochemistry and Molecular Biophysics; Bioenergetics (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Cell Biology; Conservation; Development; Enzymology (Biochemistry and Molecular Biophysics); General Life Studies; Genetics; Metabolism; Methods and Techniques; Nutrition; Systematics and Taxonomy
IT Chemicals & Biochemicals
ETHANOL; ALCOHOL; **XYLOSE**; CELLULOSE
IT Industry
biotechnology industry
IT Miscellaneous Descriptors
ALCOHOL PRODUCTION; CELLULOSE CONVERSION; ENZYMES; **ETHANOL PRODUCTION**; FERMENTATION; GENETIC METHODS; GROWTH; NUTRITION; **XYLOSE** UTILIZATION
ORGN Super Taxa
Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungi (Fungi - Unspecified); fungus (Fungi - Unspecified)
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants
RN **64-17-5 (ETHANOL)**
64-17-5 (ALCOHOL)
58-86-6Q (XYLOSE)
25990-60-7Q (XYLOSE)
9004-34-6 (CELLULOSE)

L133 ANSWER 10 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1994:209525** BIOSIS
DN **PREV199497222525**
TI Fed-batch fermentation of **xylose** by a fast-growing mutant of **xylose**-assimilating recombinant **Saccharomyces cerevisiae**.
AU Tantirungkij, Manee; Izuishi, Tamaki; Seki, Tatsuji; Yoshida, Toshiomi (1)
CS (1) International Cent. Cooperative Res. Biotechnol., Fac. Eng., Osaka Univ., 2-1, Yamada-oka, Suita-shi, Osaka 565 Japan
SO Applied Microbiology and Biotechnology, (1994) Vol. 41, No. 1, pp. 8-12. ISSN: 0175-7598.
DT Article
LA English
AB Mutants of **xylose**-assimilating recombinant **Saccharomyces cerevisiae** carrying the **xylose reductase** and **xylitol dehydrogenase** genes on plasmid pEXGD8 were selected, after ethyl methanesulfonate treatment, for their rapid growth on **xylose** medium. The fastest growing strain (strain IM2) showed a lower activity of **xylose reductase** but a higher ratio of **xylitol dehydrogenase** to **xylose reductase** activities than the parent strain, as well as high **xylulokinase** activity. Southern hybridization of the chromosomal DNA indicated that plasmid pEXGD8 was integrated into the chromosome of mutant IM2, resulting in an increase in the stability of the cloned genes. In batch fermentation under O-2 limitation, the yield and production rate of **ethanol** were improved 1.6 and 2.7 times, respectively, compared to the parent strain. In fed-batch culture with slow feeding of **xylose** and appropriate O-2 supply at a low level, xylitol excreted

from the cells was limited and the **ethanol** yield increased 1.5 times over that in the batch culture, with a high initial concentration of **xylose**, although the production rate was reduced. The results suggested that slow conversion of **xylose** to xylitol led to a lower level of intracellular xylitol, resulting in less excretion of xylitol, and an increase in the **ethanol** yield. It was also observed that the oxidation of xylitol was strongly affected by the O-2 supply.

CC Cytology and Cytochemistry - Plant *02504
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504
Comparative Biochemistry, General *10010
Biochemistry - Gases *10012
Biochemical Methods - General *10050
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biophysics - General Biophysical Studies *10502
Biophysics - Molecular Properties and Macromolecules *10506
Enzymes - General and Comparative Studies; Coenzymes *10802
Enzymes - Methods *10804
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Energy and Respiratory Metabolism *13003
Metabolism - Carbohydrates *13004
Nutrition - Carbohydrates *13220
Microbiological Apparatus, Methods and Media *32000
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Morphology, Anatomy and Embryology of Plants *51000
Plant Physiology, Biochemistry and Biophysics - Nutrition *51504
Plant Physiology, Biochemistry and Biophysics - Respiration, Fermentation *51508
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods *51524
Plant Physiology, Biochemistry and Biophysics - General and Miscellaneous *51526

BC **Ascomycetes *15100**

IT Major Concepts
Biochemistry and Molecular Biophysics; Bioenergetics (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Cell Biology; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques; Morphology; Nutrition; Physiology

IT Chemicals & Biochemicals
XYLOSE; ETHANOL; ALCOHOL; OXYGEN

IT Miscellaneous Descriptors
ALCOHOL PRODUCTION; BIOTECHNOLOGY; ENZYME ACTIVITIES; **ETHANOL PRODUCTION;** GENES; GENETICS; METHODS; OXYGEN SUPPLY; SUGAR; YIELD

ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae

ORGN Organism Name
fungus (Fungi - Unspecified); **Saccharomyces cerevisiae (Ascomycetes)**

ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants

RN **58-86-6Q (XYLOSE)**
25990-60-7Q (XYLOSE)
64-17-5 (ETHANOL)
64-17-5 (ALCOHOL)

7782-44-7 (OXYGEN)

L133 ANSWER 11 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1993:185492** BIOSIS
DN **PREV199395095942**
TI Construction of **xylose**-assimilating **Saccharomyces cerevisiae.**
AU Tantirungkij, Manee; Nakashima, Noriyuki; Seki, Tatsuji (1); Yoshida, Toshiomi
CS (1) Internatioanl Cent. Cooperative Res. Biotechnol., Fac. Eng., Osaka Univ. 2-1 Yamadaoka, Suita Osaka 565 Japan
SO Journal of Fermentation and Bioengineering, (1993) Vol. 75, No. 2, pp. 83-88.
ISSN: 0922-338X.
DT Article
LA English
AB The **xylose reductase** gene originating from Pichia stipitis was subcloned on an expression vector with the enolase promoter and terminator from **Saccharomyces cerevisiae**. The transformants of **S. cerevisiae** harboring the resultant plasmids produced **xylose reductase** constitutively at a rate about 3 times higher than P. stipitis, but could not assimilate **xylose** due to the deficient conversion of xylitol to **xylose**. The **xylitol dehydrogenase** gene was also isolated from the gene library of P. stipitis by plaque hybridization using a probe specific for its expressions of the **xylose reductase** and **xylitol dehydrogenase** genes in **S. cerevisiae** were achieved by introducing both genes on the same or coexisting plasmids. The transformants could grow on a medium containing **xylose** as the sole carbon source, but **ethanol production** from **xylose** was less than that by P. stipitis and a significant amount of xylitol was excreted into the culture broth.
CC **Genetics and Cytogenetics - Plant *03504**
Comparative Biochemistry, General 10010
Biochemical Methods - General 10050
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Methods - Carbohydrates *10058
Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biochemical Studies - Carbohydrates 10068
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Enzymes - General and Comparative Studies; Coenzymes 10802
Enzymes - Methods *10804
Enzymes - Chemical and Physical 10806
Enzymes - Physiological Studies 10808
Metabolism - Carbohydrates *13004
Metabolism - Proteins, Peptides and Amino Acids *13012
Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
Nutrition - Carbohydrates 13220
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Nutrition 51504
Plant Physiology, Biochemistry and Biophysics - Growth, Differentiation 51510
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - General and Miscellaneous *51526

BC **Ascomycetes *15100**
IT Major Concepts
Biochemistry and Molecular Biophysics; Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Metabolism; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics); Physiology
IT Industry
biotechnology industry
IT Miscellaneous Descriptors
ENZYMES; EXPRESSION VECTOR; GENES; GENETIC ENGINEERING; GENETICS; GROWTH; PROMOTER; SUGAR CONVERSIONS; TERMINATOR; TRANSFORMANTS; YIELD
ORGN Super Taxa
Ascomycetes: Fungi, Plantae; Fungi - Unspecified: Fungi, Plantae
ORGN Organism Name
fungus (Fungi - Unspecified); **yeast** (Fungi - Unspecified); **Pichia stipitis (Ascomycetes); Saccharomyces cerevisiae (Ascomycetes)**
ORGN Organism Superterms
fungi; microorganisms; nonvascular plants; plants

L133 ANSWER 12 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN **1992:325515** BIOSIS
DN **BA94:27356**
TI ISOLATION AND CHARACTERIZATION OF ACETIC ACID-TOLERANT GALACTOSE-FERMENTING STRAINS OF **SACCHAROMYCES-CEREVISIAE** FROM A SPENT SULFITE LIQUOR FERMENTATION PLANT.
AU LINDEN T; PEETRE J; HAHN-HAEGERDAL B
CS APPLIED MICROBIOLOGY, CHEM. CENTER, LUND UNIVERSITY, P.O. BOX 124, S-221 00 LUND, SWEDEN.
SO APPL ENVIRON MICROBIOL, (1992) 58 (5), 1661-1669.
CODEN: AEMIDF. ISSN: 0099-2240.
FS BA; OLD
LA English
AB From a continuous spent sulfite liquor fermentation plant, two species of **yeast** were isolated, **Saccharomyces cerevisiae** and Pichia membranaefaciens. One of the isolates of **S. cerevisiae**, no. 3, was heavily flocculating and produced a higher **ethanol** yield from spent sulfite liquor than did commercial baker's **yeast**. The greatest differeces between isolate 3 and baker's **yeast** was that of galactose fermentation, even when galactose utilization was induced, i.e., when they were grown in the presence of galactose, prior to fermentation. Without acetic acid present, both baker's **yeast** and isolate 3 fermented **glucose** and galactose sequentially. Galactose fermentation with baker's **yeast** was strongly inhibited by acetic acid at pH values below 6. Isolate 3 fermented galactose, **glucose**, and mannose without catabolite repression in the presence of acetic acid, even at pH 4.5. The **xylose reductase** (EC 1.1.1.21) and **xylitol dehydrogenase** (EC 1.1.1.9) activities were determined in some of the isolates as well as in two strains of **S. cerevisiae** (ATCC 24860 and baker's **yeast**) and Pichia stipitis CBS 6054. The **S. cerevisiae** strains manifested **xylose reductase** activity that was 2 orders of magnitude less than the corresponding P. stiptis value of 890 nmol/min/mg of protein. The **xylose** dehydrogenase activity was 1 order of magnitude less than the corresponding activity of P. stipitis (330 nmol/min/mg of protein).
CC **Genetics and Cytogenetics - Plant 03504**
Comparative Biochemistry, General 10010
Biochemical Methods - General *10050
Biochemical Studies - General 10060
Biochemical Studies - Carbohydrates 10068
Enzymes - General and Comparative Studies; Coenzymes 10802

Enzymes - Physiological Studies *10808
Metabolism - General Metabolism; Metabolic Pathways *13002
Metabolism - Carbohydrates *13004
Microbiological Apparatus, Methods and Media 32000
Public Health: Environmental Health - Sewage Disposal and Sanitary Measures 37014
Food and Industrial Microbiology - Biosynthesis, Bioassay and Fermentation *39007
Plant Physiology, Biochemistry and Biophysics - Enzymes *51518
Plant Physiology, Biochemistry and Biophysics - Metabolism *51519
Plant Physiology, Biochemistry and Biophysics - Chemical Constituents *51522
Plant Physiology, Biochemistry and Biophysics - Apparatus and Methods 51524
BC **Ascomycetes 15100**
IT Miscellaneous Descriptors
PICHIA-MEMBRANAEFACIENS PICHIA-STIPITIS BAKER'S **YEAST**
XYLOSE REDUCTASE EC 1.1.1.21 **XYLITOL**
DEHYDROGENASE EC 1.1.1.9 **GLUCOSE** FERMENTATION
CATABOLIC REPRESSION NEGATIVE LIGNOCELLULOSIC SUBSTRATE UTILIZATION
ETHANOL PRODUCTION SYNTHETIC METHOD BIOTECHNOLOGY
RN **50-99-7** (**GLUCOSE**)
64-17-5 (**ETHANOL**)
64-19-7 (ACETIC ACID)
9028-31-3 (EC 1.1.1.21)
14265-45-3 (SULFITE)

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L154 ANSWER 1 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 2002-097582 [13] WPIX
DNC C2002-030382
TI Obtaining recombinant yeast of **Saccharomyces cerevisiae** for fermenting lignocellulose raw materials to **ethanol**, comprises introducing deoxyribonucleic acid into yeast.
DC D16 D17 E17
IN CORDERO OTERO, R R; HAHN-HAEGERDAL, B; VAN ZYL, W H

PA (FORS-N) FORSKARPATENT I SYD; (FORS-N) FORSKARPATENT I SYD AB
CYC 96
PI WO 2001088094 A1 20011122 (200213)* EN 18p C12N001-19
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2001058985 A 20011126 (200222) C12N001-19
EP 1282686 A1 20030212 (200312) EN C12N001-19
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
ADT WO 2001088094 A1 WO 2001-SE1061 20010515; AU 2001058985 A AU 2001-58985 20010515; EP 1282686 A1 EP 2001-932462 20010515, WO 2001-SE1061 20010515
FDT AU 2001058985 A Based on WO 200188094; EP 1282686 A1 Based on WO 200188094
PRAI ZA 2000-2363 20000515
IC ICM C12N001-19
ICS C12P007-10
AB WO 200188094 A UPAB: 20020226
NOVELTY - Obtaining recombinant yeast of **Saccharomyces cerevisiae**, comprising introducing DNA into a yeast, where the obtained yeast introduces genes encoding **xylose reductase**, xylithol dehydrogenase and **xylulokinase**, is new.
USE - For obtaining recombinant yeast of **Saccharomyces cerevisiae** useful for fermenting lignocellulose raw materials to produce **ethanol**.
ADVANTAGE - The obtained recombinant yeast is efficiently capable of fermenting lignocellulose raw materials to produce **ethanol**.
Dwg.0/2
FS CPI
FA AB; DCN
MC CPI: D05-B03; D05-C03B; D05-H05; D05-H08; D05-H12A; D05-H17A3; E10-E04E2
TECH UPTX: 20020226
TECHNOLOGY FOCUS - BIOLOGY - Preferred Product: The yeast is capable of producing one or more lignocellulose utilizing enzymes of **xylose reductase**, xylithol dehydrogenase, or **xylulokinase**.
Preferred Enzymes: The enzymes of the yeast is of the genus **Saccharomyces cerevisiae** and Pichia stipitis. The **xylose reductase** or **xylitol dehydrogenase** lignocellulose utilizing enzyme can be obtained from Pichia stipitis. The **xylulokinase** enzyme is obtained from **Saccharomyces cerevisiae**. Preferred Medium: The growth medium by the recombinant yeast comprises **glucose** and **xylose**. Preferred Method: The method includes isolating mutants by ethyl methanesulfonate treatment. The mutants show a growth rate over basic strain of more than 30%. The recombinant strain is maintained in continuous culture on **xylose** as carbon source at dilution rate of 0.1/h with growth rate on **xylose** of 0.14-0.15/h and biomass yield of 0.4 g/g on **xylose** at aerobic growth. It utilizes 20 g/L and 15-16 g/L of **xylose** (4-5 g/L residual) in a continuous culture from a 20 g/L **xylose** and 20 g/L of **glucose** feed. Preferred Strain: The **Saccharomyces cerevisiae** strain is **Saccharomyces cerevisiae** USM21, which has been deposited under CBS 102678. It is (non-)detoxified lignocellulose hydrolysates, or (soft or hard)wood derived hydrolysate. Preferred Mutants: The mutant is a **xylose**-fermenting mutant XYLUSM125, which is deposited under CBS 102679 or XYLUSM145, which is deposited under CBS 102680.
ABEX UPTX: 20020226
EXAMPLE - XYLUSM125 mutant was grown in 20 g/L **xylose** in minimal medium and established XYLUSM125 in a continuous culture on 20 g/L

xylose using dilution rate of 0.1/h (aerobic fermentation condition). The growth rate obtained on **xylose** as carbon source was 0.14-0.15/h and the biomass yield was 0.4 g/g to have 8 g/L biomass on 20 g/L **xylose** as carbon source. When the feed was changed to 20 g/L **xylose** and 20 g/L **glucose** the biomass had raised to 18 g/L and the result was only 4-5 g/L **xylose** remained. The XYLUSM125 mutant utilized 20 g/L **glucose** and 15-16 g/L **xylose** in continuous fermentation.

L154 ANSWER 2 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1999-418470** [35] WPIX
DNC **C1999-122944**
TI Production of **ethanol** and 1,2-propanediol.
DC A41 B05 D16 D21 D25 E17 G04
IN CAMERON, D C; HOFFMAN, M L; SHAW, A J
PA (WISC) WISCONSIN ALUMNI RES FOUND
CYC 82
PI WO 9928481 A1 19990610 (199935)* EN 48p C12N015-60 <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW
AU 9916107 A 19990616 (199945) C12N015-60 <--
ADT WO 9928481 A1 WO 1998-US25318 19981130; AU 9916107 A AU 1999-16107 19981130
FDT AU 9916107 A Based on WO 9928481
PRAI **US 1997-984717 19971203**
IC ICM **C12N015-60**
ICS C12N001-19; C12N009-88; **C12N015-81**; C12P007-18; C12P007-26
ICI C12P007-18, C12R001:685; C12N001-19, C12R001:685
AB WO 9928481 A UPAB: 19990902
NOVELTY - A new method for the production of **ethanol** and 1,2-propanediol comprises using a genetically modified yeast which expresses suitable enzymes, particularly an E. coli methylglyoxal synthase (MGS)

DETAILED DESCRIPTION - (A) A novel genetically-engineered yeast (GEY) expresses one or more recombinant enzymes which enables the GEY to produce **ethanol**, 1,2-propanediol (1,2-PD), or both in isolatable quantities.

INDEPENDENT CLAIMS are also included for:

(1) a method of producing a compound selected from **ethanol**, 1,2-PD, or a combination, comprising culturing a GEY which expresses one or more recombinant enzymes which enable the GEY to produce **ethanol**, 1,2-PD, or both, in a medium containing a carbon substrate utilizable by the yeast;

(2) a method of producing a compound selected from **ethanol**, 1,2-PD, or combinations comprising culturing a GEY as in (A) in a medium containing a carbon source selected from arabinose, galactose, lactose, sucrose, **xylose**, starch and combinations, whereby the carbon source is fermented into **ethanol** and 1,2-PD;

(3) a synthetic operon which enables the production of 1,2-PD and **ethanol** in yeast transformed to contain the operon, the operon comprising one or more genes whose encoded gene products catalyze the formation of methylglyoxal in yeast and a promoter sequence functional in yeast operationally linked to the one or more genes;

(4) a synthetic operon functional in yeast comprising a sequence (V) shown (7065 nucleotides in length).

USE - The products and methods can be used for the production of 1,2-PD which can be used in the production of unsaturated polyester resins, liquid laundry detergents, pharmaceuticals, cosmetics, antifreeze and deicing formulations. They can also be used to produce

ethanol. The byproducts of fermentation are carbon dioxide, alcohols, and organic acids, all of which can be purified as valuable co-products or used as animal feed.

ADVANTAGE - The microbial process can use as a substrate a renewable sugar such as **glucose, xylose** or lactose or products from corn and cane sugar and from lignocellulosic biomass. The process produces no toxic wastes and does not involve high temperatures and pressures. The process can produce high yields, of the order of about 1.0 moles or more of **ethanol** or 1,2-PD per mole sugar.

Dwg.0/8

FS CPI
FA AB; DCN
MC CPI: A01-E14; B10-E04D; B11-A02; D05-C03G; D05-H05; D05-H08; D05-H14A2; D05-H17A3; D08-B; D11-A; D11-B02; E10-E04B; E10-E04F; G04-B01; G04-B05
TECH UPTX: 19990902
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferably the GEY expresses a recombinant E. coli methylglyoxal synthase.
ABEX UPTX: 19990902
EXAMPLE - The DNA coding region for E. coli methylglyoxal synthase (MGS) was amplified by PCR. The PCR product was inserted, using restriction enzymes, into the expression vector YpJ66. YpJ66 is based on YEp352 and contains the CUP1 promoter and the CYC1 terminator for the expression of proteinis in **S. cerevisiae**. The product pMH36 was used to transform yeast strain YPH500. An overnight culture of YPH500 yeast transformed with plasmid pMH36 was grown in SDM for 24 hours. Aliquots (0.1ml each) of this culture were then inoculated into a series of 10ml cultures of SDM containing various levels of copper (0-0.6mM) (in addition to the copper already present in the SDM and allowed to ferment in anaerobic tubes for 60 hours at 30degreesC. At a copper concentration of 0.15mM the amount of 1,2-propandiol produced was 0.21g/l.

L154 ANSWER 3 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1999-347189 [29] WPIX
DNC C1999-102120
TI New microorganism having modified carbohydrate metabolism and/or fermentation capacity comprising recombinant DNA capable of expressing trehalose phosphate phosphatase.
DC D11 D16 E17
IN GODDIJN, O J M; PEN, J
PA (MOGE-N) MOGEN INT NV
CYC 82
PI WO 9923225 A1 19990514 (199929)* EN 28p C12N015-54 <--
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW
AU 9915597 A 19990524 (199940) C12N015-54 <--
ADT WO 9923225 A1 WO 1998-EP7009 19981030; AU 9915597 A AU 1999-15597 19981030
FDT AU 9915597 A Based on WO 9923225
PRAI **EP 1997-203372 19971030**
IC ICM **C12N015-54**
ICS A21D008-04; C12C011-00; C12N001-19; **C12N015-55**
AB WO 9923225 A UPAB: 19990723
NOVELTY - The microorganism has a modified carbohydrate metabolism and/or fermentation capacity characterized in that it comprises a recombinant DNA capable of expressing trehalose phosphate phosphatase (TPP).

DETAILED DESCRIPTION - The microorganism may also comprise an alteration caused by a recombinant DNA expressing product expressing a product which influences the endogenous level of trehalos-6-phosphate, the product preferably selected from the group consisting of TPS, TPP,

trehalase, trehalose phosphate, trehalose phosphorylase and antisense trehalase.

INDEPENDENT CLAIMS are also included for:

(1) the use of the above microorganism in a fermentation process;

(2) a dough comprising the above microorganism;

(3) a method for baking using the above dough;

(4) bread or any other bakery product using the dough as above;

(5) a method for the production of alcohol using the above microorganism;

(6) a method for producing an alcoholic beverage using the above microorganism;

(7) a beer or other alcoholic beverage using the above method;

(8) a microorganism deposited under number CBS 922.97 at the central bureau of Schimmelcultures on July 7, 1997; and

(9) a method for producing the microorganism.

USE - The microorganism is useful for fermentation processes especially for dough in bakery products, for **ethanol** production and for brewing beer and other alcoholic beverages (all claimed).

ADVANTAGE - The microorganism has increased fermentation capacity therefore producing an improved dough. The TPP transgenic yeast strain was tested in a preparation of dough. The strains were then precultured in aerobic, sugar limited chemostat cultures. The control produced 7.1 mMol **ethanol**/g biomass/hour and the TPP transgenic yeast produced 9.5 mMol **ethanol**/g biomass/hour when incubated for 5-30 minutes.

Dwg.0/1

FS CPI

FA AB; DCN

MC CPI: D01-B02; E10-E04E2; E11-M

TECH UPTX: 19990723

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preparation: The method for producing a microorganism having a modified carbohydrate metabolism and/or fermentation capacity characterized in that the microorganism is transformed with recombinant DNA capable of expression of an expression product which influences the endogenous level of trehalose-6-phosphate. Preferred Microorganism: The recombinant DNA is heterologous, e.g. bacterial, fungal, plant, animal or human DNA, especially Escherichia coli. The yeast is preferably a strain of **Saccharomyces**, especially **Saccharomyces cerevisiae**.

ABEX UPTX: 19990723

EXAMPLE - Precultures were prepared by inoculating 100 ml mineral medium (0.3% w/v **glucose**) with 1 ml frozen sock culture. The cultures were incubated on an orbital shaker (200 rpm) at 30 degreesC for 1 day. For growth curves, 4 ml preculture was inoculated in a flask with 100 ml minerl medium and then shaken at 30 degreesC. Optical density measurements were performed.

L154 ANSWER 4 OF 18 WPIX (C) 2003 THOMSON DERWENT

AN 1999-244034 [20] WPIX

DNC C1999-071220

TI Yeast strain transformed with lactic dehydrogenase gene.

DC A41 B04 B05 D13 D16 E17

IN ALBERGHINA, L; BIANCHI, M; FRONTALI, L; PORRO, D; RANZI, B M; VAI, M; WINKLER, A A; ABERGHINA, L

PA (BIOP-N) BIOPOLO SCARL; (STAL) STALEY MFG CO A E

CYC 83

PI WO 9914335 A1 19990325 (199920)* EN 85p C12N015-53 <--

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

AU 9895392 A 19990405 (199933) C12N015-53 <--

EP 1012298 A1 20000628 (200035) EN C12N015-53 <--
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI
BR 9812434 A 20000926 (200051) C12N015-53 <--
IT 1294728 B 19990412 (200157) C12N000-00
JP 2001516584 W 20011002 (200172) 85p C12N015-09 <--
MX 2000002436 A1 20010601 (200235) C07K014-395
AU 748462 B 20020606 (200249) C12N015-53 <--
US 6429006 B1 20020806 (200254) C12N001-14
US 2003032152 A1 20030213 (200314) C12P007-40

ADT WO 9914335 A1 WO 1998-EP5758 19980911; AU 9895392 A AU 1998-95392 19980911; EP 1012298 A1 EP 1998-948950 19980911, WO 1998-EP5758 19980911; BR 9812434 A BR 1998-12434 19980911, WO 1998-EP5758 19980911; IT 1294728 B **IT 1997-MI2080 19970912**; JP 2001516584 W WO 1998-EP5758 19980911, JP 2000-511873 19980911; MX 2000002436 A1 MX 2000-2436 20000309; AU 748462 B AU 1998-95392 19980911; US 6429006 B1 WO 1998-EP5758 19980911, US 2000-508277 20000629; US 2003032152 A1 Cont of WO 1998-EP5758 19980911, Cont of US 2000-508277 20000629, US 2002-68137 20020206

FDT AU 9895392 A Based on WO 9914335; EP 1012298 A1 Based on WO 9914335; BR 9812434 A Based on WO 9914335; JP 2001516584 W Based on WO 9914335; AU 748462 B Previous Publ. AU 9895392, Based on WO 9914335; US 6429006 B1 Based on WO 9914335

PRAI **IT 1997-MI2080 19970912**

IC ICM C12N000-00; C12N001-14; **C12N015-09**; **C12N015-53**; C12P007-40
ICS C12N001-18; C12N001-19; C12N009-04; C12P007-56

ICA C07K014-395; **C12N015-31**

ICI C07K014:395, **C12N015-31**; C12N001-19; C12N001-19; C12P007-56; C12R001:645; C12R001:645; C12R001:865

AB WO 9914335 A UPAB: 20011203

NOVELTY - Yeast strain unable to produce **ethanol**, or producing it at lower level than the wild type, is transformed with at least one copy of the gene (I) for lactic dehydrogenase (LDH) linked to a promoter functional in yeast, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) vector containing (I) linked to a pyruvate decarboxylase (PDC) gene promoter; and

(2) production of lactic acid by culturing the new strains.

ACTIVITY - None given.

MECHANISM OF ACTION - Both ethanolic fermentation and utilization of pyruvate by mitochondria are replaced by lactic fermentation.

USE - The yeast strains are cultured to produce lactic acid, in D- and/or L- forms, and the residual biomass is useful e.g. as animal feed. Lactic acid, and its derivatives, are useful in chemistry, cosmetics, pharmaceuticals, food manufacture and for production of biodegradable polymers.

ADVANTAGE - The yeast's produce lactic acid with high yield, productivity and selectivity, e.g. yields of over 80 wt.% based on **glucose** consumed. They can be grown under acid conditions (this minimizes contamination by other microbes and ensures that lactic acid is present mainly as free acid, reducing the need for conversion to, and isolation of lactate salts); may be recovered for reuse; are suitable for continuous fermentation processes and non-conventional carbon sources may be used. **Saccharomyces cerevisiae** strain GRF18U (in which the PCD2 gene for pyruvate decarboxylase was inactivated) was transformed with the integrative plasmids pLC5, containing the LDH gene from Lactobacillus casei, modified for compatibility with yeast and pJEN1 encoding the lactate transporter of **S. cerevisiae**. In batch cultures these cells produced 6.06 g/l lactate and only 4.23 g/l **ethanol**; comparable figures for cells transformed with pLC5 only were 3.33 and 4.39 g/l.

Dwg.0/11

FS CPI
FA AB; DCN
MC CPI: A01-E12; B04-F09; B10-C04D; B14-R01; D03-G02; D05-A04; D05-C09; D05-H08; D05-H12A; D05-H12B2; D05-H12C; D05-H14A2; D05-H17A6; E10-C04D4
TECH UPTX: 19990517
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred yeast: These have **ethanol** producing capacity less than 60% of that of the wild type and also have reduced activity of PDC and/or pyruvate dehydrogenase (PDH). Particularly the genes for PDC and/or PDH are disrupted by deletion or insertion of a selectable marker, particularly the URA3 marker of **Saccharomyces cerevisiae** or a dominant marker that encodes resistance to a toxic compound.
Preferred yeast are **S. cerevisiae**, Kluyveromyces lactis, Torulaspora delbreuckii or Zygosaccharomyces bailii, and they are transformed with (I) encoding bovine or bacterial LDH, particularly by integration into the yeast genome from an expression vector containing the K. lactis promoter. Typically transformed cells contain 10-50 copies of (I). Optionally the new cells also overexpress the lactate transporter JEN1.
Process: To produce lactic acid, the yeast are cultured on a medium containing **glucose**, fructose, galactose, lactose, sucrose, raffinose, maltose, cellobiose, arabinose or **xylose**. The medium contains less than 5 mM magnesium ions and/or less than 0.02 mM zinc ions, and has pH 7 or lower, particularly 3 or lower. The process produces the D- or L- lactic acid or a mixture of the two.
ABEX UPTX: 19990517
EXAMPLE - The PM6-7A strain of Kluyveromyces lactis, (see Yeast, 8 (1992) 711), was modified by deletion of the K1PDCA gene (encoding pyruvate decarboxylase) by inserting the URA3 marker of **Saccharomyces cerevisiae**. Transformants were selected on medium containing 5-fluoro-orotic acid to isolate the ura-negative mutant PHI/C1, which does not produce **ethanol** and can be grown on **glucose** -containing media. This strain was transformed, by electroporation, with the replicable vector pEPL2 which contains the bovine lactate dehydrogenase gene under control of the K1PDCA promoter, also the URA3 marker. The transformants were grown on minimal medium, buffered with pH 5.6 phosphate, and they produced lactate at 11.4 g/l, with 90% of this as free acid.

L154 ANSWER 5 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1997-480563** [44] WPIX
DNC **C1997-152705**
TI Novel strain of **Saccharomyces cerevisiae** - can be used in fermenting sugars to **ethanol** for industrial and potable purposes.
DC D16 E17 H06
IN CHAKRABARTI, T; MONDAL, A K; PRASAD, G S
PA (COUL) CSIR COUNCIL SCI IND RES
CYC 4
PI ZA 9602541 A 19970827 (199744)* 20p C12N000-00 <--
EP 798382 A1 19971001 (199744)# EN 8p C12P007-06 <--
R: FI GB
US 5693526 A 19971202 (199803)# 6p C12N001-16 <--
ADT ZA 9602541 A **ZA 1996-2541 19960329**; EP 798382 A1 **EP 1996-302227 19960329**; US 5693526 A **US 1996-625000 19960329**
PRAI **ZA 1996-2541 19960329**; **EP 1996-302227 19960329** ; **US 1996-625000 19960329**
REP 2.Jnl.Ref; FR 2616445; US 4910144
IC ICM C12N000-00; C12N001-16; C12P007-06
ICS C12N001-19; **C12N015-04**
ICI C12N001-19, C12R001:865; C12P007-06, C12R001:8
AB ZA 9602541 A UPAB: 19971105

A novel strain (I) of yeast **Saccharomyces cerevisiae**, accession number MTCC Y0022B211 (NCYC 2647), is of use for preparation of **ethanol** by fermentation of sugars.

Also claimed is the preparation of (I) by: (a) growing diploid strain of **S.cerevisiae** MTCC Y0001 (NCYC 2646), sporulating conventionally, treating the sporulated cells with a lytic enzyme and collecting the liberated spores; (b) growing haploid strain of **S. cerevisiae** MTCC Y0002 (ATTC 90506) and collecting the cells (B) in a conventional medium; (c) mixing collected spores and cells, and incubating at 15-37 deg.C for 1-10 days; (d) spreading the mixture over a non-selective medium and incubating at 15-37 deg.C for 1-10 days; (e) collecting the cells produced and spreading over a selective medium to eliminate spores/cells from steps (a) and (b), allowing only hybrid cells/cytoductants to grow; and (f) purifying the latter conventionally.

USE - (I) may be used for production of potable or industrial **ethanol**.

ADVANTAGE - (I) is more osmo-tolerant and **ethanol** tolerant than prior strains, permitting production of a higher level of **ethanol** and higher initial concentration of sugars; overall less sugars are utilised and effluent volume and steam consumption are reduced; the cells flocculate and sediment when agitation is stopped.

Dwg.0/0

FS CPI
FA AB; DCN
MC CPI: D05-B03; D05-H14A2; E10-E04E2; E11-M; H06-B
ABEQ US 5693526 A UPAB: 19980119

A novel strain (I) of yeast **Saccharomyces cerevisiae**, accession number MTCC Y0022B211 (NCYC 2647), is of use for preparation of **ethanol** by fermentation of sugars.

Also claimed is the preparation of (I) by: (a) growing diploid strain of **S.cerevisiae** MTCC Y0001 (NCYC 2646), sporulating conventionally, treating the sporulated cells with a lytic enzyme and collecting the liberated spores; (b) growing haploid strain of **S. cerevisiae** MTCC Y0002 (ATTC 90506) and collecting the cells (B) in a conventional medium; (c) mixing collected spores and cells, and incubating at 15-37 deg.C for 1-10 days; (d) spreading the mixture over a non-selective medium and incubating at 15-37 deg.C for 1-10 days; (e) collecting the cells produced and spreading over a selective medium to eliminate spores/cells from steps (a) and (b), allowing only hybrid cells/cytoductants to grow; and (f) purifying the latter conventionally.

USE - (I) may be used for production of potable or industrial **ethanol**.

ADVANTAGE - (I) is more osmo-tolerant and **ethanol** tolerant than prior strains, permitting production of a higher level of **ethanol** and higher initial concentration of sugars; overall less sugars are utilised and effluent volume and steam consumption are reduced; the cells flocculate and sediment when agitation is stopped.

Dwg.0/0

L154 ANSWER 6 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1995-368626 [48] WPIX
DNC C1995-160292
TI New cellobiase from Cellulomonas biazotea and related nucleic acid - used to degrade cellulosic waste, esp. to **ethanol** in conjunction with yeast glucanase(s).
DC D16 E17 H06
IN CHAN, W K; WONG, W K
PA (UYHK-N) UNIV HONG KONG
CYC 1
PI GB 2289050 A 19951108 (199548)* 41p C12N015-56 <--
GB 2289050 B 19980826 (199836) C12N015-56 <--
ADT GB 2289050 A **GB 1995-9237 19950505**; GB 2289050 B **GB 1995-9237 19950505**

PRAI **GB 1994-9030 19940506**
IC ICM **C12N015-56**
ICS C12N001-22; C12N009-24; C12P007-10
ICA C12N001-19
ICI C12R001:865; C12N001-22; **C12N015-56**, C12R001:865
AB GB 2289050 A UPAB: 19951204
Cellobiase (I) from Cellulomonas biazotea and its recombinant forms, including variants and enzymatically active fragments, are new.
USE - (I) is useful for degrading cellulosic substrates, e.g. waste paper, opt. used with other cellulose-degrading enzymes. Esp. new strains of **S. cerevisiae** containing (I) can be used to convert cellulose to **ethanol**, via **glucose**.
ADVANTAGE - Recombinant (I) can be produced on a large scale as an extracellular enzyme. Since it is relatively free of contaminating protein it has high specific activity.
Dwg.0/14
FS CPI
FA AB; DCN
MC CPI: D05-H12A; D05-H12E; D05-H14; D05-H14A2; D05-H16A; D05-H17A3; E10-E04E2; E11-M; H06-B

L154 ANSWER 7 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1995-194082 [25] WPIX
DNC C1995-089834
TI Recombinant yeast encoding **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase** - can effectively ferment **xylose** alone, or simultaneously with **glucose**, to produce **ethanol** e.g. for use as a fuel.
DC D16 E17 H06
IN HO, N W Y; TSAO, G T
PA (PURD) PURDUE RES FOUND
CYC 59
PI WO 9513362 A1 19950518 (199525)* EN 63p C12N001-14
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ
W: AM AU BB BG BR BY CA CN CZ EE FI GE HU JP KG KP KR KZ LK LR LT LV MD MG MN NO NZ PL RO RU SI SK TJ TT UA UZ VN
AU 9510517 A 19950529 (199537) C12N001-14
EP 728192 A1 19960828 (199639) EN C12N001-14
R: AT BE DE DK ES FR GB GR IE IT NL SE
FI 9601926 A 19960704 (199641) C12N000-00
BR 9408010 A 19961217 (199705) C12N001-14
JP 09505469 W 19970603 (199732) 56p C12N015-09
US 5789210 A 19980804 (199838) C12P007-08
AU 695930 B 19980827 (199846) C12N001-14
CN 1141057 A 19970122 (200047) C12N001-14
ADT WO 9513362 A1 WO 1994-US12861 19941108; AU 9510517 A AU 1995-10517 19941108; EP 728192 A1 WO 1994-US12861 19941108, EP 1995-901176 19941108; FI 9601926 A WO 1994-US12861 19941108, FI 1996-1926 19960507; BR 9408010 A BR 1994-8010 19941108, WO 1994-US12861 19941108; JP 09505469 W WO 1994-US12861 19941108, JP 1995-513948 19941108; US 5789210 A US 1993-148581 19931108; AU 695930 B AU 1995-10517 19941108; CN 1141057 A CN 1994-194767 19941108
FDT AU 9510517 A Based on WO 9513362; EP 728192 A1 Based on WO 9513362; BR 9408010 A Based on WO 9513362; JP 09505469 W Based on WO 9513362; AU 695930 B Previous Publ. AU 9510517, Based on WO 9513362
PRAI US 1993-148581 19931108
REP 4.Jnl.Ref
IC ICM C12N000-00; C12N001-14; C12N015-09; C12P007-08
ICS C07H021-04; C12N001-19; C12N009-00; C12N009-02; C12N009-12; C12N015-00; C12N015-81; C12P007-06
ICI C12N015-09, C12R001:865; C12N001-19, C12R001:865; C12P007-06, C12R001:865
AB WO 9513362 A UPAB: 19951128
Recombinant yeast (pref. of the genus **Saccharomyces**) contains

introduced genes (pref. fused to non-**glucose**-inhibited promoters) encoding **xylose reductase**, **xylitol dehydrogenase** (XD) and **xylulokinase** effective for fermenting **xylose** to **ethanol**. Also claimed are: (1) a recombinant DNA molecule comprising genes encoding **xylose reductase**, XD and **xylulokinase**; and (2) a vector for transforming yeast comprising these genes.

USE - The yeast can effectively ferment **xylose**, alone or simultaneously with **glucose**, to produce **ethanol**; the **ethanol** can be used as liq. fuel for cars either as a neat fuel (100% **ethanol**) or as a blend with petroleum.

ADVANTAGE - The recombinant yeast are suitable for **ethanol** fuel production by fermentation using plant biomass as feedstock.

Dwg.0/14

FS CPI
FA AB; GI; DCN
MC CPI: D05-B03; D05-H12C; D05-H12E; D05-H14A2; D06-B; E10-E04E2; E11-N; H06-B

L154 ANSWER 8 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1993-404008 [50] WPIX
CR 1987-150624 [21]
DNC C1993-179594
TI Increasing prodn. of carbon di oxide and **ethanol** in yeast - by increasing cellular ATP metabolism or introducing cytoplasmic acid phosphatase activity.
DC D11 D16 E17 E36
IN ROGERS, D T; SZOSTAK, J W
PA (GEMY) GENETICS INST INC
CYC 1
PI US 5268285 A 19931207 (199350)* 41p C12N015-63 <--
ADT US 5268285 A **CIP of US 1985-796551 19851108, Cont of US 1987-85099 19870707, CIP of US 1990-533992 19900604, US 1991-733472 19910722**
PRAI **US 1985-796551 19851108; US 1987-85099 19870707 ; US 1990-533992 19900604; US 1991-733472 19910722**
IC ICM **C12N015-63**
ICS C12N001-19
AB US 5268285 A UPAB: 19940203
The rate of CO2 and **ethanol** prodn. of **Saccharomynces** is increased by: (a) transforming the yeast with DNA encoding yeast frustose-1,6-diphosphatase (I) controlled by a **Saccharomyced** promoter from the galactose, maltose, phosphate, nitrogen metabolism, isocytochrome or alcohol dehydrogenase II gene protomers, and (b) inducing the expression of the DNA during growth on **glucose** by activating the promoter.

Pref. the rate of CO2 and **ethanol** prodn. may also be increased by genetically modifying yeast DNA encoding an exocellular acid phosphatase, to cause the enzyme to remain in the yeast cytoplasm and catalyse the controlled hydrolysis of intraceullular ATP. The modification is the deletion of a functional secretory leader sequence from the DNA.

Pref. the DNA encoding (I) is mutated such that codon 12 of the mutagenised DNA encodes Ala, Thr, Val or Cys. The promoter is temp. sensitive. The regulable promoter permits constitutive expression of the DNA.

USE/ADVANTAGE - Prodn. rates are increased by reducing the ATP level of the cell by substitution of a regulable promoter for a natural promoter, e.g. of the (I) gene. This may be done via a single copy of a multicopy vector or via cointegration into the yeast genome. This allows regulable expression of the enzyme at the same time as the reverse reaction such that ATP is consumed, e.g. (I) expression during cell growth on **glucose**. This stimulated glycolysis is accomplished by

inducing these ATP-consuming cycles or by introducing cytoplasmic acid phosphatase activity. The genetic modifications may be turned on only during, and pref. at the early stage of the levening phase and not during the prodn.-level growth of the cell. Alternatively, they may be constitutively expressed so they are turned on during large scale prodn., e.g. commerical scale growth of the yeast for enhanced prodn. levels. Dwg.0/23

FS CPI
FA AB; DCN
MC CPI: D01-B01; D05-H05; D05-H12; E10-E04E2; E11-M; E31-N05C

L154 ANSWER 9 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1991-325230 [44] WPIX
DNC C1991-140554
TI DNA encoding **xylose reductase** and/or **xylitol dehydrogenase** - useful for transforming yeast strains for expression of one enzyme or co-expression of both.
DC B05 D13 D16 E17 F09
IN AIRAKSINEN, U; HAHN-HAGERDAL, B; HALLBORN, J; KERANEN, S; OJAMO, H; PENTTILA, M; WALFRIDSSON, M; HAHN-HAEGERDAL, B; KERAENEN, S; PENTTILAE, M; HAHNHAGERD, B; WALFRIDSSO, M
PA (VALW) VALTION TEKNILLINEN TUTKIMUSKESKUS; (XYRO-N) XYROFIN OY; (VALW) VALTION TEKNILLINEN; (HALL-I) HALLBORN J
CYC 20
PI

WO 9115588	A	19911017 (199144)*		47p		
RW: AT BE CH DE DK ES FR GB GR IT LU NL SE						
W: AU CA FI JP NO US						
AU 9175657	A	19911030 (199205)				
FI 9204461	A	19921002 (199302)			C12N000-00	
NO 9203880	A	19921006 (199306)			C12N015-53	
EP 527758	A1	19930224 (199308)	EN		C12N015-53	
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE						
JP 05507843	W	19931111 (199350)		17p	C12N015-53	
AU 647104	B	19940317 (199416)			C12N015-53	
EP 527758	B1	19980107 (199806)	EN	24p	C12N015-53	
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE						
DE 69128619	E	19980212 (199812)			C12N015-53	
ES 2113373	T3	19980501 (199824)			C12N015-53	
US 5866382	A	19990202 (199912)			C12P007-02	
FI 9902153	A	19991006 (200003)			C12N000-00	
FI 104636	B1	20000315 (200020)			C12N015-53	
NO 308544	B1	20000925 (200056)			C12N015-53	
CA 2090122	C	20020618 (200250)	EN		C12N015-53	
JP 3348215	B2	20021120 (200282)		21p	C12P007-18	

ADT FI 9204461 A WO 1991-FI103 19910408, FI 1992-4461 19921002; NO 9203880 A WO 1991-FI103 19910408, NO 1992-3880 19921006; EP 527758 A1 EP 1991-906996 19910408, WO 1991-FI103 19910408; JP 05507843 W JP 1991-506907 19910408, WO 1991-FI103 19910408; AU 647104 B AU 1991-75657 19910408; EP 527758 B1 EP 1991-906996 19910408, WO 1991-FI103 19910408; DE 69128619 E DE 1991-628619 19910408, EP 1991-906996 19910408, WO 1991-FI103 19910408; ES 2113373 T3 EP 1991-906996 19910408; US 5866382 A CIP of US 1990-527775 19900524, Cont of US 1992-848694 19920309, US 1994-336198 19941103; FI 9902153 A WO 1991-FI103 19910408, Div ex FI 1992-4461 19921002, FI 1999-2153 19991006; FI 104636 B1 WO 1991-FI103 19910408, FI 1992-4461 19921002; NO 308544 B1 WO 1991-FI103 19910408, NO 1992-3880 19921006; CA 2090122 C CA 1991-2090122 19910408, WO 1991-FI103 19910408; JP 3348215 B2 JP 1991-506907 19910408, WO 1991-FI103 19910408
FDT EP 527758 A1 Based on WO 9115588; JP 05507843 W Based on WO 9115588; AU 647104 B Previous Publ. AU 9175657, Based on WO 9115588; EP 527758 B1 Based on WO 9115588; DE 69128619 E Based on EP 527758, Based on WO 9115588; ES 2113373 T3 Based on EP 527758; FI 104636 B1 Previous Publ. FI 9204461; NO 308544 B1 Previous Publ. NO 9203880; CA 2090122 C Based on WO 9115588; JP 3348215 B2 Previous Publ. JP 05507843, Based on WO 9115588

PRAI FI 1990-1771 19900406
REP 7.Jnl.Ref
IC ICM C12N000-00; C12N015-53; C12P007-02; C12P007-18
ICS C12N001-19; C12N015-52; C12N015-81; C12P007-06; C12P019-02
ICA C12N009-04; C12N015-09
ICI C12P007-18, C12R001:865
AB WO 9115588 A UPAB: 19991215
DNA (I) encoding **xylose reductase** enzyme (A) is new.
When (I) is transferred into a yeast strain it renders the strain capable of reducing **xylose** to **xylitol**.
Pref. the yeast of (1) is capable of integrating to the yeast chromosome when transformed into a yeast strain. (I) and/or (II) is expressed under yeast gene regulatory regions, e.g. promoters of (A), (B), yeast alcohol dehydrogenase gene ADH1 or yeast phosphoglycerate kinase gene PGK1, and functional fragments. The yeast strain is a **Saccharomyces cerevisiae** strain (pref.), kluyveromyces strain, Schizosacchoromyces pombe strain or Pichia strain.
The yeast vectors pUA103, pUA107, pJHXR22, pMW22, pJHXDH60 and pJHXDH70, and the yeast strains. S. cerivisiae H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.
USE - The yeast transformants can reduce xylase to **xylitol** for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a yeast strain results in the prodn. of **ethanol**.
Dwg.0/8
FS CPI
FA AB; DCN
MC CPI: B04-B02B2; B04-B02C2; B04-B04A1; B10-A07; B10-E04D; B11-A; B12-J01; B12-L03; D05-B03; D05-C03B; D05-C03D; D05-H03B; D05-H12; E10-A07; F05-A02C; F05-B
ABEQ EP 527758 A UPAB: 19930928
DNA (I) encoding **xylose reductase** enzyme (A) is new.
When (I) is transferred into a yeast strain it renders the strain capable of reducing **xylose** to **xylitol**.
Pref. the yeast of (1) is capable of integrating to the yeast chromosome when transformed into a yeast strain. (I) and/or (II) is expressed under yeast gene regulatory regions, e.g. promoters of (A), (B), yeast alcohol dehydrogenase gene ADH1 or yeast phosphoglycerate kinase gene PGK1, and functional fragments. The yeast strain is a **Saccharomyces cerevisiae** strain (pref.), kluyveromyces strain, Schizosaccharomyces pombe strain or Pichia strain.
The yeast vectors pUA103, pUA107, pJHXR22, pMW22, pJHXDH60, and pJHXDH70, and the yeast strains S. cerivisiae H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.
USE - The yeast transformants can reduce xylase to **xylitol** for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a yeast strain results in the prodn. of **ethanol**
ABEQ EP 527758 B UPAB: 19980209
DNA (I) encoding **xylose reductase** enzyme (A) is new.
When (I) is transferred into a yeast strain it renders the strain capable of reducing **xylose** to **xylitol**.
Pref. the yeast of (1) is capable of integrating to the yeast chromosome when transformed into a yeast strain. (I) and/or (II) is expressed under yeast gene regulatory regions, e.g. promoters of (A), (B), yeast alcohol dehydrogenase gene ADH1 or yeast phosphoglycerate kinase gene PGK1, and functional fragments. The yeast strain is a **Saccharomyces cerevisiae** strain (pref.), kluyveromyces strain, Schizosacchoromyces pombe strain or Pichia strain.
The yeast vectors pUA103, pUA107, pJHXR22, pMW22, pJHXDH60 and pJHXDH70, and the yeast strains. S. cerivisiae H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.

USE - The yeast transformants can reduce xylase to **xylitol** for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a yeast strain results in the prodn. of **ethanol**. Dwg.0/8

L154 ANSWER 10 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1991-296506 [41] WPIX
DNC C1991-128227
TI New DNA encoding **xylose reductase** and **xylitol dehydrogenase** - and transformed yeast for prodn. of **ethanol** and biomass from **xylose** or recovery of oxidised NADP.
DC B02 B04 D16 E17
IN AMORE, R; HAGEDORN, J; HOLLENBERG, C P; KOTTER, P; PIONTEK, M; STRASSER, A W M; VONCIRIACY, M; KOETTER, P; VON, CIRIACY-WANTRUP M; HAGENDORN, J
PA (RHEI-N) RHEIN BIOTECH NEUE BIOTECHNOLOGISCHE PROZESSE & PROD GMBH; (RHEI-N) RHEIN BIOTECH GES NEUE BIOTECHNOLOGISCHE; (RHEI-N) RHEIN BIOTECH GES B; (RHEI-N) RHEIN BIOTECH GMBH
CYC 16
PI DE 4009676 A 19911002 (199141)* 50p
EP 450430 A 19911009 (199141) 50p
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE
CA 2039021 A 19910927 (199150)
EP 450430 A3 19920102 (199320) 50p
DE 4009676 C2 19930909 (199336) 51p C12N001-19
JP 06339383 A 19941213 (199509) 32p C12N015-53
EP 450430 B1 19970625 (199730) EN C12N015-53
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE
DE 69126632 E 19970731 (199736) C12N015-53
ES 2104626 T3 19971016 (199748) C12N015-53
JP 2000139486 A 20000523 (200033) 21p C12N015-09
JP 3122153 B2 20010109 (200104) 32p C12N015-09
JP 2001103988 A 20010417 (200128) 27p C12N015-09
JP 3193917 B2 20010730 (200146) 27p C12N015-09
ADT DE 4009676 A DE 1990-4009676 19900326; EP 450430 A EP 1991-104558 19910322; EP 450430 A3 EP 1991-104558 19910322; DE 4009676 C2 DE 1990-4009676 19900326; JP 06339383 A JP 1991-62160 19910326; EP 450430 B1 EP 1991-104558 19910322; DE 69126632 E DE 1991-626632 19910322, EP 1991-104558 19910322; ES 2104626 T3 EP 1991-104558 19910322; JP 2000139486 A Div ex JP 1991-62160 19910326, JP 2000-589 19910326; JP 3122153 B2 JP 1991-62160 19910326; JP 2001103988 A Div ex JP 1991-62160 19910326, JP 2000-276227 19910326; JP 3193917 B2 Div ex JP 1991-62160 19910326, JP 2000-276227 19910326
FDT DE 69126632 E Based on EP 450430; ES 2104626 T3 Based on EP 450430; JP 3122153 B2 Previous Publ. JP 06339383; JP 3193917 B2 Previous Publ. JP 2001103988
PRAI DE 1990-4009676 19900326
REP NoSR.Pub; 6.Jnl.Ref; EP 238023; GB 2151635; JP 60199383; JP 61063291; US 4840903
IC C07H021-04; C07K015-04; C12C011-00; C12N001-19; C12N009-02; C12N015-63; C12P007-06; C12P019-34
ICM C12N001-19; C12N015-09; C12N015-53
ICS C07H021-04; C07K013-00; C07K015-04; C12C011-00; C12N001-14; C12N001-21; C12N009-02; C12N009-04; C12N015-63; C12N015-81; C12P007-06; C12P007-10; C12P019-34; C12P021-02
ICI C12N009-02; C12N009-02; C12N015-09; C12N015-09; C12N015-09; C12R001:645; C12R001:84; C12R001:84; C12R001:85; C12R001:865; C12N001-19; C12N001-19; C12N001-19; C12N001-21; C12N009-04; C12N015-09; C12P007-06; C12P007-06; C12P007-06; C12P007-06; C12R001:01; C12R001:01; C12R001:645; C12R001:645; C12R001:84; C12R001:84; C12R001:84; C12R001:84; C12R001:865; C12R001:865; C12N001-19, C12R001:865; C12N009-02, C12R001:865; C12P007-06, C12R001:865; C12N015-53, C12R001:645; C12N001-19, C12R001:865; C12N009-02,

C12R001:865

AB DE 4009676 A UPAB: 19971030

New DNA sequence (I) comprises a structural gene encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

Also new are (1) combinations of (I) with other DNA halogen sequences for regulating expression; (2) vectors and microorganisms contg. (I), and (3) XR and XDH produced by expressing (I).

More specifically, (I) is derived from a yeast, specifically Pichia stipitis CBS 5773 (DSM 5855). The specification includes sequences for DNA fragments which encode XR (2040 bases) and XDH (1950 bases), and the derived structures (318 and 363 amino acids, respectively).

USE/ADVANTAGE - XR and XDH are useful (1) for prodn. of **ethanol** from **xylose** (a waste prod. of cellulose mfr.); (2) for prodn. of biomass and (3) for recovery of NADP(+) for NADPH. The microorganisms transformed with (I) can ferment highly conc. carbohydrate solns. prior art and are tolerant to **EtOH**, pH and temp.. Also contemplated is prodn. of specific proteins (II) in P. stipitis by expressing the structural gene for (II) under control of the 5'-regulatory region of the XR and XDH genes of P. stipitis (these are inducible by **xylose**) and/or the ADH1 promoter of **S. cerevisiae** and/or the glucoamylase promoter of Schwanniomyces occidentalis. P. Stipitis has an efficient secretory system and can use **xylose** as a C source. @(50pp Dwg.No.0/7)

FS CPI

FA AB; DCN

MC CPI: B04-B02B2; B04-B02C2; B04-B04A1; D05-C03B; D05-H03B; D05-H05; D05-H12; E10-E04E2

ABEQ EP 450430 A UPAB: 19931113

New DNA sequence (I) comprises a structural gene encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

Also new are (1) combinations of (I) with other DNA halogen sequences for regulating expression; (2) vectors and microorganisms contg. (I), and (3) XR and XDH produced by expressing (I).

More specifically, (I) is derived from a yeast, specifically Pichia stipitis CBS 5773 (DSM 5855). The specification includes sequences for DNA fragments which encode XR (2040 bases) and XDH (1950 bases), and the derived structures (318 and 363 amino acids, respectively).

USE/ADVANTAGE - XR and XDH are useful (1) for prodn. of **ethanol** from **xylose** (a waste prod. of cellulose mfr.); (2) for prodn. of biomass and (3) for recovery of NADP(+) for NADPH. The microorganisms transformed with (I) can ferment highly conc. carbohydrate solns. prior art and are tolerant to **EtOH**, pH and temp.. Also contemplated is prodn. of specific proteins (II) in P. stipitis by expressing the structural gene for (II) under control of the 5'-regulatory region of the XR and XDH genes of P. stipitis (these are inducible by **xylose**) and/or the ADH1 promoter of **S. cerevisiae** and/or the glucoamylase promoter of Schwanniomyces occidentalis. P. Stipitis has an efficient secretory system and can use **xylose** as a C source. @(50pp Dwg.No.0/7)

ABEQ DE 4009676 C UPAB: 19931122

Recombinant DNA sequence that encodes the prodn. of an xylosereductase and/or xylitoldehydrogenase has been utlised in expression vectors contg. this DNA to produce the enzymes. Host cells have been transformed with these vectors and then propagated to produce the exogenous polypeptides. The nucleotide sequence of the cDNA and the aminoacid sequences of the polypeptides are defined.

USE - The prods. facilitate the degradation of **xylose** from wood pulp, leading to the conversion of waste biomass to alcohol. Dwg.0/7

ABEQ EP 450430 B UPAB: 19970723

New DNA sequence (I) comprises a structural gene encoding a **xylose**

reductase (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

L154 ANSWER 11 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1989-041102** [06] WPIX
DNC **C1989-017951**
TI **Ethanol** prepn. - using high resistance microorganism strain, belonging to **Saccharomyces cerevisiae** diploid homo-thallic strain.
DC D16 E17
IN SORA, S; SPROCATI, A R
PA (CNEN) ENEA-COM NAZ ENERG
CYC 2
PI FR 2616445 A 19881216 (198906)* 11p <--
IT 1206039 B 19890405 (199130) <--
ADT FR 2616445 A **FR 1988-7909 19880614**
PRAI **IT 1987-48059 19870615**
IC C12N001-16; **C12N015-00**; C12P007-06; C12R001-86
AB FR 2616445 A UPAB: 19930923
In the prepn. of **ethanol** by means of high resistance microorganisms strains, the fermentation stock comprising the starting material is treated with microorganisms belonging to a **Saccharomyces cerevisiae** diploid homothallic strain, obtd. by passing through selection cycles, a mutageneous premeistical treatment designed to introduce a genetic variability and successive selections, that strain having the property to resist high concns. of **ethanol**, not to be inhibited at high concns. of **glucose** of up to 30% wt./vol. and to produce **ethanol** at concns. reaching up to 15% w/vol.
The **Saccharomyces cerevisiae** MI 861/10 is used, and is deposited under No. DSM 4128 at Deutsche Sammlung von Microorganism of Gottingen. The fermentation stock contains **glucose** (30% w/v) and molasses (above 2.5 w/v, pref. 7.5-10%).
ADVANTAGE - The obtd. prod. is richer in **ethanol** compared to prods. obtd. in prior art.
0/0
FS CPI
FA AB; DCN
MC CPI: D05-B03; E10-E04E2

L154 ANSWER 12 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1988-333480 [47] WPIX
DNC C1988-147235
TI Glucoamylase producing transformed yeast - cultured by recombining glucoamylase gene of rhizopus in chromosome deoxyribonucleic acid of host yeast, to reveal glucoamylase gene.
DC D16
PA (SUNR) SUNTORY LTD
CYC 1
PI JP 63245664 A 19881012 (198847)* 9p <--
JP 2607509 B2 19970507 (199723) 11p C12N001-19 <--
ADT JP 63245664 A **JP 1987-78301 19870331**; JP 2607509 B2 **JP 1987-78301 19870331**
FDT JP 2607509 B2 Previous Publ. JP 63245664
PRAI **JP 1987-78301 19870331**
IC C12N001-16; C12N009-34
ICM C12N001-19
ICS C12N001-16; **C12N015-09**; C12P007-06
ICA C12N009-34
AB JP 63245664 A UPAB: 19930923
Transformed yeast is induced by recombining the glucoamylase gene originated from Rhizopus, stably in the chromosome DNA of host yeast so that glucoamylase gene is revealed. As host yeast the yeast strain

showing **ethanol** productivity can be pref. used and practically **Saccharomyces** strains can be pref. used. Glucoamylase gene is produced by glucoamylase-producing Rhizopus. For recombing glucoamylase gene, YRp-type recombining vector (pYGA195X) and YIp-type recombing vector (e.g. pIGA3201, pIG3202, pIGA3203, pIGA3204 and pIGA3205) can be used. By recombining glucoamylase gene in parent strain, the productivity for glucoamylase can be increased and glucoamylase productivity is increased parallel to the number of the copies recombined. Yeast strain recombined with more copies does not show high alcohol-fermentating property and the number of copies is so selected that it depends on object of preparing glucoamylase or saccharification. The recombined yeast strain G-1315 has two copies and shows high alcohol productivity. Thus induced G5-2T strain is trusted to the Institute for microbial industry FERM P-1321.

USE/ADVANTAGE - Glucoamylase has been used for saccharifying starch by preparing **glucose, ethanol**, etc. Glucoamylase has been prepd. from Rhizopus by solid culture. By the invented method the transformed yeast strain can be cultured by liq. culture and by using it **ethanol** can be prepd. from starch by single process.

0/1

FS CPI
FA AB
MC CPI: D05-B04; D05-C03C; D05-H05

L154 ANSWER 13 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1988-285168** [40] WPIX
DNC **C1988-126673**
TI Genetically stable **Saccharomyces** diastaticus fusion prod - useful in prodn. of fuel alcohol(s).
DC D16 H06
IN PANCHAL, C J; RUSSELL, I; STEWART, G G
PA (LABA-N) LABATT BREWING CO LTD
CYC 1
PI US 4772556 A 19880920 (198840)* 9p <--
ADT US 4772556 A **US 1986-883421 19860714**
PRAI **US 1983-532158 19830914; US 1986-883421 19860714**
IC C12N001-18; **C12N015-00**; C12P007-06; C12R001-85
AB US 4772556 A UPAB: 19930923

Saccharomyces diastaticus strain NCYC 1460 is new. A biologically pure culture of the strain is also claimed, as is a novel genome comprising a multiple non-allelic dextrin gene complement, which is the genome present in cells of NCYC 1460. In the prodn. of fuel alcohol from a fermented mash, the improVement comprises fermenting the mash with S. diastaticus strain NCYC 1460.

One fusion partner was a respiratory deficient mutant corresp. to a hybrid diploid strain of S. diastaticus which was unable to grow in lactate media. Thisstrain exhibited growth at 37 deg. C, was unable to ferment melibiose and it was homozygous recessive in respect of maltose-related genes. The second fusion partner was a strain of S. uvarum (carlsbergensis) which was capable of growth on lactate media and which fermented melibiose. This strain would not grow at 37 deg. C nor was it capable of fermenting dextrins. ADVANTAGE - Strain NCYC 1460, which is a fusion prod., shows high osmotolerance than its parent strains. This characteristic is highly desirable in industrial yeast utilised in fuel alcohol prodn. where efficient fermentation must often be carried out in high gravity substrates. The strain is an efficient **EtOH** producer, capable of fermenting **glucose** at 40 deg. C and ordinarily very genetically stable.

0/9

FS CPI
FA AB
MC CPI: D05-B03; D05-H05; D05-H08; D05-H12; H06-B01

L154 ANSWER 14 OF 18 WPIX (C) 2003 THOMSON DERWENT

AN **1986-044936** [07] WPIX
DNC **C1986-018790**
TI Yeast glucoamylase gene - from **saccharomyces** genus of yeast.
DC B04 D16
PA (MITK) MITSUI TOATSU CHEM INC
CYC 1
PI JP 60262593 A 19851225 (198607)* 15p <--
JP 05069510 B 19931001 (199342) 14p C12N015-55 <--
ADT JP 60262593 A **JP 1984-116636 19840608**; JP 05069510 B **JP 1984-116636 19840608**
FDT JP 05069510 B Based on JP 60262593
PRAI **JP 1984-116636 19840608**
IC C12N001-16; C12N009-34; **C12N015-00**; C12P007-06; C12P019-20
ICM **C12N015-55**
ICS C12N001-16; C12P007-06; C12P019-20
ICA C12N009-34
ICI **C12N015-55**, C12R001:85
AB JP 60262593 A UPAB: 19930922
DNA sequence contains region coding promotor region concerning manifestation of gene, ribosome-bonding region in **Saccharomyces** genus of yeast, region concerning exosecretin of protein synthesised as result of manifestation and region coding aminoacid sequence of enzyme protein. It originates from glucoamylase gene of **Saccharomyces** genus of yeast, e.g. one of **Saccharomyces** geasticus.
0/0
FS CPI
FA AB
MC CPI: B04-B02B2; B04-B02C3; B04-B04A1; B10-A07; B10-E04D; D05-B03; D05-B04; D05-C03C; D05-C08
ABEQ JP 93069510 B UPAB: 19931202
DNA sequence contains region coding promotor region concerning manifestation of gene, ribosome-bonding region in **Saccharomyces** genus of yeast, region concerning exosecretin of protein synthesised as result of manifestation and region coding aminoacid sequence of enzyme protein. It originates from glucoamylase gene of **Saccharomyces** genus of yeast, e.g. one of **Saccharomyces** geasticus.
(J60262593-A)

L154 ANSWER 15 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1985-276144** [44] WPIX
DNC **C1985-119969**
TI Yeast strains producing cellulolytic enzyme(s) - are obtd. by recombinant DNA methods for use in brewing, pharmaceuticals prodn., wood pulp and paper industries etc..
DC B04 D16 F09
IN KNOWLES, J; LEHTOVAARA-HELENIUS, P; NEVALAINEN, H; PENTTILAE, M; SALOVUORI, I; TEERI, T; PENTTILA, M; SALOVUROI, I; NEVALAINEN, H M K; AHO, S; KERAENEN, S; NITISINPRASERT, S; PALOHEIMO, M
PA (ALKO-N) ALKO OY AB; (KNOW-I) KNOWLES J; (VALW) VALTION TEKNILLINEN; (ALKO-N) ALKO-YHTIOT OY
CYC 12
PI WO 8504672 A 19851024 (198544)* EN 42p <--
RW: AT BE DE FR GB NL SE
W: DK FI SU US
EP 214971 A 19870325 (198712) EN <--
R: AT BE DE FR GB NL SE
FI 8604110 A 19861010 (198727) <--
DK 8505803 A 19851213 (198731) <--
EP 312121 A 19890419 (198916) EN <--
R: AT BE DE FR GB NL SE
US 4894338 A 19900116 (199010) <--
CA 1305931 C 19920804 (199237) C12N015-56 <--
US 5393670 A 19950228 (199514) 24p C12N001-21 <--

EP 214971 B1 19950412 (199519) EN 28p C12N015-82 <--
R: AT BE DE FR GB NL SE
DE 3588008 G 19950518 (199525) C12N015-82 <--
US 5529919 A 19960625 (199631) 25p C12N009-42 <--
US 5766915 A 19980616 (199831) C12N009-42

ADT WO 8504672 A **WO 1985-FI39 19850412**; EP 214971 A **EP 1985-902041 19850412**; EP 312121 A **EP 1988-118230 19850412**; US 4894338 A **US 1986-817942 19860130**; CA 1305931 C **CA 1985-478959 19850412**; US 5393670 A **Div ex US 1986-817942 19860130, Cont of US 1989-418154 19891006, US 1993-95253 19930723**; EP 214971 B1 **EP 1985-902041 19850412, WO 1985-FI39 19850412**; DE 3588008 G **DE 1985-3588008 19850412, EP 1985-902041 19850412, WO 1985-FI39 19850412**; US 5529919 A **Cont of WO 1985-FI39 19850412, Div ex US 1986-817942 19860130, Cont of US 1989-418154 19891006, Cont of US 1993-95253 19930723, US 1994-264492 19940623**; US 5766915 A **Div ex WO 1985-FI39 19850412, Div ex US 1986-817942 19860130, CIP of US 1989-418154 19891006, Cont of US 1991-801161 19911129, US 1995-380438 19950130**

FDT US 5393670 A Div ex US 4894338; EP 214971 B1 Based on WO 8504672; DE 3588008 G Based on EP 214971, Based on WO 8504672; US 5529919 A Div ex US 4894338, Cont of US 5393620; US 5766915 A Div ex US 4894338

PRAI **FI 1984-1500 19840413**

REP 1.Jnl.Ref; AT 3118; AU 8287238; AU 8312152; CA 1151089; DE 2953253; DE 3308215; EP 100254; EP 11767; EP 73635; EP 88632; FR 2523152; FR 2529569; GB 2116567; JP 58077896; JP 58174396; US 4275163; WO 8001080; WO 8400175; 2.Jnl.Ref; 6.Jnl.Ref; A3...8950; EP 137280; No-SR.Pub

IC ICM C12N001-21; C12N009-42; **C12N015-56**; **C12N015-82**
ICS C07H021-00; C07K007-00; C12N001-00; C12N001-19; **C12N015-00**; **C12N015-52**; **C12N015-70**; **C12N015-81**

AB WO 8504672 A UPAB: 19960705

DNA sequence coding for a fungal cellulase enzyme, or its single or multiple base substitutions is new. It is derived from natural synthetic or semisynthetic sources. It is capable, when correctly combined with an expression vector, of expressing a non-native protein having cellulolytic activity on transformation of a host organism by the vector. The DNA sequence codes for a defined sequence of 421 amino acid residues or a portion of it.

Signal sequence responsible for the secretion of proteinaceous material extracellularly and having the amino acid residue sequence of formulae (I) or (II) is new.

Recombinant DNA vector comprising a DNA sequence or signal sequence as defined above, is new, the vector being able to replicate and express in a suitable host organism. Yeast strain contg. a DNA sequence or signal sequence as defined above, or a chromosomal gene or cDNA sequence coding for cellobiohydrolase I is new. It is esp. **Saccharomyces cerevisiae** VTT-RC-84001 (NCYC R112), -84011, -84012 or -84013.

USE/ADVANTAGE - The yeast strains constructed can produce celluloytic enzymes and so they would give improved results when cultured in presence of cellulose or glucans. They may be used in brewing, wine making, baking, **EtOH** prodn., single cell protein prodn., and in the prodn. of pharmaceuticals such as interferon, growth hormone and hepatitis B virus antigen. Beer produced with the yeasts could be filtered and clarified more easily and more economically. Yeast strains producing only one cellulase may be useful in the wood pulp and paper industry.

0/10

Dwg.0/10

FS CPI

FA AB

MC CPI: B02-V; B04-B02B; B04-B02C3; B04-B04A; B04-B04C; B04-C01; D05-B; D05-E; D05-H03; D05-H07; F05-A02A

ABEQ US 4894338 A UPAB: 19930925

DNA sequence and its active fragments have been isolated and cloned from the fungus Trichoderma reesei, and opt. modified by substn., deletion, insertion, or inversion of one or more bases. These DNA sequences encode the prodn. of mature cellobiohydrolase-II when incorporated in expression vectors in host microorganisms, e.g. **Saccharomyces cerevisiae**.

USE - The exogenous enzyme hydrolyses cellulose, and provides an easy means of treating cellulose and beta-glucans during beer fermentation.

ABEQ US 5393670 A UPAB: 19950412

Recombinant DNA encodes the prodn. of a polypeptide having the aminoacid sequence of mature endoglucanase-I. The nucleotide sequence of the cDNA and the aminoacid sequence of the polypeptide are defined. Plasmids and expression vectors contg. this DNA are new. Host cells have been transformed with these vectors and then propagated to produce the exogenous polypeptide.

USE - The process facilitates the prodn. of cellulolytic enzymes from transformed yeasts.

ADVANTAGE - The enzyme hydrolyses 3-1,4-glucan substrates, e.g. cellulose, and supports the fermentative prodn. of **glucose**, etc. from cellulose sources.

Dwg.0/11

ABEQ EP 214971 B UPAB: 19950524

A DNA sequence which codes for the cellulase enzyme cellobiohydrolase II from Trichoderma reesei which is capable, when correctly combined with an expression vector, of expressing a protein having the cellulolytic activity of the said enzyme upon transformation of a host organism by the vector, said DNA sequence coding for the amino acid sequence defined in the specification contg. 471 aminoacids or for a substantially identical amino acid sequence showing the same enzymatic activity.

Dwg.0/7

ABEQ US 5529919 A UPAB: 19960808

A new method for producing endoglucanase I, said method comprising transforming a host with DNA encoding the endoglucanase I amino acid sequence of FIGS. 6 or 11 (as given in the specification) and producing said endoglucanase I protein.

Dwg.0/11

L154 ANSWER 16 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1985-105155** [18] WPIX
DNC **C1985-045687**
TI Prodn. of fuel alcohol(s) from fermentable mash - by using **Saccharomyces** diastaticus NCYC 1460.
DC D16 E17 H06
IN PANCHAL, C J; RUSSEL, I; STEWART, G G
PA (LABA-N) LABATT BREWING CO LTD
CYC 8
PI AU 8431949 A 19850314 (198518)* 20p <--
EP 139114 A 19850502 (198518) EN <--
R: DE FR GB NL
JP 60145086 A 19850731 (198537) <--
CA 1199593 A 19860121 (198608) <--
EP 139114 B 19890222 (198908) EN <--
R: DE FR GB NL
DE 3476817 G 19890330 (198914) <--
JP 07024577 B2 19950322 (199516) 7p C12N001-19 <--
ADT AU 8431949 A **AU 1984-31949 19840815**; EP 139114 A **EP 1974-108823 19740825**; JP 60145086 A **JP 1984-188768 19840907** ; EP 139114 B **EP 1984-108823 19840725**; JP 07024577 B2 **JP 1984-188768 19840907**
FDT JP 07024577 B2 Based on JP 60145086
PRAI **CA 1983-436141 19830907**
REP 4.Jnl.Ref; A3...8622; GB 1212437; No-SR.Pub; US 2415734
IC C12N001-16; **C12N015-00**; C12P007-06; C12R001-85

ICM C12N001-19
ICS C12N001-16; **C12N015-02**; C12R001-85
ICA C12P007-06
ICI C12N001-19, C12R001:85; C12P007-06, C12R001:
AB AU 8431949 A UPAB: 19930925
Saccharomyces diastaticus NCYC 1460 is new. Biologically pure culture of S. diastaticus NCYC 1460 is new. Novel genome comprising a multiple non-allelic dextrin gene complement and consisting of the genome present in cells of S. diastaticus NCYC 1460 is new.
Prodn. of fuel alcohols comprises prepn. of a fermentable mash; fermenting the mash with S. diastaticus NCYC 1460; and recovery of the fuel alcohols produced.
USE/ADVANTAGE - The fuel alcohols are esp. obtd. from a mash contg. a preponderance of **glucose**, esp. when 30% by vol. of the mash is **glucose**, by use of the allopolyploid yeast strain S. diastaticus NCYC 1460. With this strain **EtOH** prodn. is greater than with its parent strains. The strain also ferments melibiose, raffinose, a large proportion of the dextrins present in a starchy mass and it rapidly ferments maltose.
0/6
FS CPI
FA AB
MC CPI: D05-B; D05-H; E10-E04E; H06-B
ABEQ EP 139114 B UPAB: 19930925
A novel strain of **Saccharomyces** diastaticus, strain NCYC 1460.

L154 ANSWER 17 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN **1982-04576J** [48] WPIX
TI Fermenting D-**xylose** to **ethanol** - using specific yeast mutants with high conversion efficiency.
DC D16 D17 E17
IN GONG, C S
PA (PURD) PURDUE RES FOUND; (PURO) PUROLATOR INC
CYC 20
PI WO 8204068 A 19821125 (198248)* EN 24p <--
W: AU BR DK FI JP NO
EP 66396 A 19821208 (198250) EN <--
R: AT BE CH DE FR GB IT LI LU NL SE
US 4368268 A 19830111 (198305) <--
ZA 8203350 A 19830427 (198329) <--
US 4511656 A 19850416 (198518) <--
EP 66396 B 19850821 (198534) EN <--
R: AT BE CH DE FR GB IT LI LU NL SE
DE 3265585 G 19850926 (198540) <--
CA 1207257 A 19860708 (198632) <--
ADT EP 66396 A **EP 1982-302474 19820514**; US 4368268 A **US 1982-376731 19820511**
PRAI **US 1981-263925 19810515; US 1981-363925 19810515 ; US 1982-376731 19820511**
REP No-SR.Pub; 5.Jnl.Ref; 2.Jnl.Ref; US 1857429; US 2288314; US 2481263; US 3880717; US 3930946; US 3954536; US 4172764; US 4288550
IC C12N001-16; **C12N015-00**; C12P007-06
AB WO 8204068 A UPAB: 19930915
Direct fermentation of D-**xylose** (I) to **ethanol** comprises inoculating a medium contg. nutrients and (I) with a yeast able to convert (I) to **ethanol** with bioconversion yield at least 50%. The mixt. is fermented until (I) conversion to **ethanol** of at least 50 (pref. 80)% is achieved. Pref. the yeast mutants Candida sp. XF217 or **Saccharomyces cerevisiae** SCXF 138 (both claimed as new microorganisms) are used. The medium contains 1-40 (5-30) wt.-vol.% (I) initially and is fermented aerobically or anaerobically at 22-40 (30) deg.C and pH 4-8 (about 6). The medium may also contain D-**glucose** (also converted) e.g. a cellulose or hemicellulose

hydrolysate.
Hemicellulose waste materials e.g. sugar cane bagasse, are available in large quantities and then mutants efficiently convert the sugar formed when they are hydrolysed.
FS CPI
FA AB
MC CPI: D05-B; D05-H03; E10-E04E
ABEQ US 4511656 A UPAB: 19930915
Prodn. of **ethanol** comprises fermentation of D-**xylose** with a parent yeast strain of Candida sp. or **Saccharomyces cerevisiiae** species, in the presence of suitable nutrients at pH about 4-8 pref. 6, and at 22-40 pref 30 deg under aerobic conditions; such that at least 50% pref. 80% of the **xylose** is converted to **EtOH**.
ADVANTAGE - Process utilises cellulose hydrolysate and/or hemicellulose hydrolysate as a nutrient medium, with conversion of both D-**glucose** and D-**xylose**.
ABEQ EP 66396 B UPAB: 19930915
A process for the direct fermentation of D-**xylose** to **ethanol** which comprises incoluating a medium comprising growth nutrients and D-**xylose** with a yeast mutant having an ability to ferment D-**xylose** to **ethanol** with a bioconversion yield of at least 50%, permitting the inoculated medium to ferment for a period of time sufficient to achieve a conversion of D-**xylose** to **ethanol** of at least 50% and recovering the **ethanol** so produced as product.

L154 ANSWER 18 OF 18 WPIX (C) 2003 THOMSON DERWENT
AN 1981-51030D [28] WPIX
TI Sparkling muscatel wine prodn. - using specified **Saccharomyces** oviformis yeast strain for intensive fermentation.
DC D16
IN ABRAMOV, S H A; KOTENKO, S T S; SARISHVILI, N G
PA (ASDA-R) AS USSR DAGESTAN
CYC 1
PI SU 773073 B 19801023 (198128)* <--
PRAI **SU 1979-2761994 19790426**
IC C12G001-06; **C12N015-00**
AB SU 773073 B UPAB: 19930915
Yeast strain **Saccharomyces** oviformis DI-4 is used for the prodn. of the sparkling muscatel wine. In a wine must, the strain forms egg-shaped cells (size 3.8-4.1 x 10.5-11.5 microns). In a must-agar medium, oval cells are formed (2.6-4.0 x 8.7-12 microns). The strain is propagated by gemmation.
This strain assimilates **glucose**, saccharose and maltose. It also assimilates **ethanol**, glycerol acetic acid, lactic acid, tartaric acid and citric acid. It also assimilates peptone, (NH4)2SO4, glycocol, urea, espargine and diphenylamine. This strain intensively ferments a muscatel must contg. 10-12% of sugar and 10-11% of alcohol (by vol.).Bul. 39/23.10.80.
FS CPI
FA AB
MC CPI: D05-B

=> d all abeq tech abex tot

L160 ANSWER 1 OF 2 WPIX (C) 2003 THOMSON DERWENT
AN 1997-558974 [51] WPIX
DNC C1997-178545
TI Yeast which ferments xylose to ethanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple reiterated ribosomal DNA sites.

DC D16 D17 E17 H06
IN CHEN, Z; HO, N W Y
PA (PURD) PURDUE RES FOUND
CYC 76
PI WO 9742307 A1 19971113 (199751)* EN 66p C12N001-16 <--
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT
SD SE SZ UG
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE
HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX
NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN YU
AU 9728301 A 19971126 (199813) C12N001-16 <--
EP 898616 A1 19990303 (199913) EN C12N001-16 <--
R: AT BE DE DK ES FI FR GB GR IE IT NL PT SE
CN 1225125 A 19990804 (199949) C12N001-16 <--
JP 2000509988 W 20000808 (200043) 50p C12N015-09 <--
MX 9809223 A1 19990701 (200061) C12N001-16
AU 731102 B 20010322 (200122) C12N001-16 <--
BR 9710963 A 20010731 (200146) C12N001-16 <--
ADT WO 9742307 A1 **WO 1997-US7663 19970506**; AU 9728301 A **AU 1997-28301 19970506**; EP 898616 A1 **EP 1997-922698 19970506, WO 1997-US7663 19970506**; CN 1225125 A **CN 1997-196195 19970506**; JP 2000509988 W **JP 1997-540153 19970506, WO 1997-US7663 19970506**; MX 9809223 A1 MX 1998-9223 19981105; AU 731102 B **AU 1997-28301 19970506**; BR 9710963 A **BR 1997-10963 19970506, WO 1997-US7663 19970506**
FDT AU 9728301 A Based on WO 9742307; EP 898616 A1 Based on WO 9742307; JP 2000509988 W Based on WO 9742307; AU 731102 B Previous Publ. AU 9728301, Based on WO 9742307; BR 9710963 A Based on WO 9742307
PRAI **US 1996-16865P 19960506**
REP 6.Jnl.Ref; WO 9513362
IC ICM C12N001-16; C12N015-09
ICS C12N001-18; C12N001-19; C12N015-68; C12N015-69; C12N015-81; C12P007-06
ICI C12N001-19; C12N001-19; C12N001-19; C12R001:72; C12R001:84; C12R001:85
AB WO 9742307 A UPAB: 19991020
Novel yeast which ferments xylose to ethanol, comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple reiterated ribosomal DNA sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol, where the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations.
USE - The methods can produce yeast, which even upon culture in non-selective medium for multiple generations, e.g. up to 20, retain their full capability to ferment xylose to ethanol.
Dwg.0/12
FS CPI
FA AB; DCN
MC CPI: D05-B03; D05-H12E; D05-H14A2; D06-G; E10-E04E2; H06-B

=> d his

(FILE 'HOME' ENTERED AT 06:47:01 ON 18 MAR 2003)
SET COST OFF

FILE 'REGISTRY' ENTERED AT 06:47:11 ON 18 MAR 2003
L1 1 S ETHANOL/CN
L2 2 S XYLOSE/CN
L3 1 S L-XYLOSE/CN

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L4            2 S GLUCOSE/CN
L5            1 S L-GLUCOSE/CN
                E XYLOSE REDUCTASE/CN
L6            4 S E3
L7           23 S XYLOSE REDUCTASE
L8           19 S L7 NOT L6
L9            4 S L6-L8 AND (SACCHAROMYCES OR CEREVISIAE)
L10          19 S L6-L8 NOT L9
                E XYLITOL DEHYDROGENASE/CN
L11           2 S E3
                E XYLITOL DEHYDROGENASE
L12           4 S XYLITOL DEHYDROGENASE
L13           2 S L12 NOT L11
                E XYLULOKINASE/CN
L14           1 S E3
                E XYLULOKINASE
L15          22 S XYLULOKINASE
L16          21 S L15 NOT L14
L17           2 S L16 AND (SACCHAROMYCES OR CEREVISIAE)
L18          20 S L14-L16 NOT L17

     FILE 'HCAPLUS' ENTERED AT 06:51:54 ON 18 MAR 2003
L19      144999 S L1
L20      497460 S ETOH OR ETHANOL OR ETHYLALCOHOL OR ETHYL ALCOHOL
L21       11773 S L2,L3
L22       23109 S XYLOSE
L23      141947 S L4 OR L5
L24      347783 S GLUCOSE
L25           7 S L9
L26        2495 S L10
L27         219 S L11 OR L12
L28           1 S L17
L29         151 S L18
L30        2747 S L25-L29
L31         427 S XYLOSE REDUCTASE OR XYLITOL DEHYDROGENASE OR XYLULOKINASE
L32        3209 S L19,L20 AND L21,L22
L33       19975 S L19,L20 AND L23,L24
L34         140 S L32,L33 AND L30,L31
L35          57 S L34 AND (SACCHAROMYCES OR S)()CEREVIS?
                E HO N/AU
L36          53 S E3,E11,E27,E30,E31
                E CHEN Z/AU
L37         669 S E3,E7
                E CHEN ZHENG/AU
L38         240 S E3,E4
L39           8 S E48
L40           3 S L35 AND L36-L39
                E GENETIC ENGINEERING/CT
                E E3+ALL
L41       79737 S E2+NT
L42      235194 S E1+NT
L43      105263 S E8+NT OR E10+NT OR E11+NT OR E16+NT OR E18+NT OR E19+NT
                E MOLECULAR CLONING/CT
                E E3+ALL
L44       68835 S E3+NT
                E E9+ALL
L45       53984 S E1+NT OR E8+NT OR E9+NT
L46      581609 S GENET?/SC,SX
L47          30 S L35 AND L41-L46
                E GENE/CT
L48      402103 S E3
                E E55+ALL
L49      551720 S E1 OR E2 OR E3+NT
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L50          29 S L35 AND L48,L49
                E NUCLEIC ACIDS/CT
                E E3+ALL
L51           2 S L35 AND E3+NT
L52           8 S L35 AND (E381+NT OR E382+NT OR E383+NT OR E384+NT OR E385+NT
                E NUCLEIC ACID SEQUENCES/CT
                E E4+ALL
L53           6 S L35 AND E4+NT
L54          36 S L47,L50-L53
L55          29 S L35 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
L56          14 S L54 AND L55
                E PROTEIN SEQUENCES/CT
                E E3+ALL
L57      218356 S E2+NT OR E9+NT
                E E10+ALL
L58        1638 S E4,E3+NT
                E E8+ALL
                E E11+ALL
L59      131970 S E2+NT OR E6+NT OR E8+NT
L60           6 S L35 AND L57-L59
L61           4 S L55 AND L60
L62          14 S L40,L56,L61
L63          43 S L35,L54-L56,L60-L61 NOT L62
L64          15 S L63 AND L55
L65          13 S L64 AND FERMENT?/SC,SX,CW,BI
L66          27 S L62,L65
L67          30 S L63 NOT L66
L68           2 S L67 AND L55
                SEL DN AN 2
L69           1 S L68 AND E1-E3
L70          28 S L66,L69
L71          29 S L67 NOT L70
L72           0 S L35 AND RIBOSOM?
L73           0 S L34 AND RIBOSOM?
L74       64238 S (S OR SACCHAROMYC?)()CEREVIS?
L75        2682 S L74 AND RIBOSOM?
                E RIBOSOME/CT
                E RIBOSOM/CT
                E E5+ALL
L76        2638 S E2
L77         124 S L76 AND L74
L78          11 S L77 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
L79        2085 S L75 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
L80          24 S L79 AND L19,L20
L81         446 S L74 AND RDNA
L82         231 S L81 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
L83           0 S L82 AND L19,L20
L84           0 S L79,L82 AND L30,L31

     FILE 'HCAPLUS' ENTERED AT 07:17:58 ON 18 MAR 2003
                SEL HIT RN L70

     FILE 'REGISTRY' ENTERED AT 07:18:36 ON 18 MAR 2003
L85          14 S E1-E14

     FILE 'HCAPLUS' ENTERED AT 07:18:48 ON 18 MAR 2003

     FILE 'BIOSIS' ENTERED AT 07:19:14 ON 18 MAR 2003
L86       58052 S L74
L87      136912 S 15100/BC
L88      115918 S YEAST
L89      479033 S FUNGI+NT/BC
L90      473655 S 15?/BC
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L91      503021 S L86-L90
L92        8439 S L19,L20 AND L91
L93        2475 S L92 AND (L2-L5 OR GLUCOSE OR XYLOSE)
L94          77 S L93 AND L30,L31
L95          55 S L94 AND PY<=1997
L96        1084 S L93 AND (10052 OR 10062 OR 035? OR 10300 OR 10511 OR 10515 OR
L97         943 S L93 AND 1080?/CC
L98         474 S L94,L97 AND L96
L99         385 S L98 AND PY<=1997
L100        231 S L99 AND L86
L101         13 S L100 AND L30,L31
L102          3 S L101 AND ALCOHOL PRODUCTION
L103          9 S L101 AND ETHANOL PRODUCTION
L104          9 S L102,L103
L105          8 S L104 NOT LIGNOCELLULOSE/TI
L106          4 S L101 NOT L104
L107         12 S L105,L106
                E HO N/AU
L108         96 S E3,E16,E20,E21
                E CHEN Z/AU
L109       1063 S E3,E6,E7
                E CHEN ZHENG/AU
L110         21 S E3
L111          6 S E27
L112         64 S L91 AND L108-L111
L113         15 S L112 AND L92
L114         21 S L112 AND (L2-L5 OR GLUCOSE OR XYLOSE)
L115         16 S L112 AND (ALCOHOL OR ETHANOL OR ETOH OR ETHYLALCOHOL OR ETHYL
L116         23 S L113-L115
L117         17 S L116 AND PY<=1997
L118         29 S L101-L107,L117
L119         43 S L112 AND  PY<=1997
L120         26 S L119 AND 035?/CC
L121         41 S L118,L120
L122         14 S L119 NOT L121
L123        155 S L100 AND 035?/CC
L124        146 S L100 AND *035?/CC
L125        143 S L123,L124 NOT L121
L126        143 S L125 AND (SACCHAROMYC? OR CEREVIS?)
L127         40 S L126 AND (ETHANOL OR ALCOHOL)(L)PRODUCTION
L128          8 S L127 AND (YIELD OR CORN STARCH OR ETHANOL PRODUCTION OR GENET
                SEL DN AN 4
L129          1 S L128 AND E1-E2
L130         42 S L121,L129
L131         20 S L130 NOT AB/FA
L132         22 S L130 NOT L131

     FILE 'BIOSIS' ENTERED AT 07:41:05 ON 18 MAR 2003
                SEL DN AN 1-12 L132
L133         12 S L132 AND E3-E26

     FILE 'WPIX' ENTERED AT 07:43:45 ON 18 MAR 2003
L134       2683 S L74/BIX
                E SACCHAROM
L135       3992 S E9,E13-E24/BIX
L136        233 S E25-E46/BIX
L137       4295 S L134-L136
L138        466 S L137 AND (ETOH OR ETHANOL OR ETHYLALCOHOL OR ETHYL ALCOHOL)/B
L139        142 S L137 AND (0245/DRN OR R00245/DCN)
L140        496 S L138,L139
L141        152 S L140 AND (GLUCOSE OR XYLOSE OR XYLITOL)/BIX
L142         38 S L140 AND ((0038 OR 0173 OR 0545)/DRN OR (R00038 OR R00173 OR
L143        158 S L141,L142
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L144          5 S L143 AND L31/BIX
L145          4 S L144 NOT ARABINOSE/TI
L146       1287 S L137 AND C12N015/IC,ICM,ICS,ICA,ICI
L147         99 S L146 AND L140
L148         42 S L147 AND L143
L149         39 S L148 NOT L144
L150         20 S L149 AND (PY<=1997 OR PRY<=1997 OR AY<=1997)
                SEL DN AN 1 4 9 11 16 17 18 19
L151          8 S L150 AND E1-E15
L152         12 S L150 NOT L151
L153          6 S L152 NOT (ANTIGEN OR RIBOFLAVIN OR HEPATITIS OR AMYLASE OR GL
L154         18 S L145,L151,L153

     FILE 'WPIX' ENTERED AT 08:10:46 ON 18 MAR 2003
L155         29 S L137 AND (HO ? OR CHEN ?)/AU
L156         28 S L155 NOT L154
L157          2 S L156 AND (HO N? OR CHEN Z?)/AU

     FILE 'HCAPLUS' ENTERED AT 08:13:03 ON 18 MAR 2003
                SEL PN APPS L40

     FILE 'WPIX' ENTERED AT 08:13:22 ON 18 MAR 2003
L158          3 S E16-E51
L159          2 S L158 NOT L154
L160          2 S L159 AND L134-L157,L158
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